

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:32:08 ; Search time 34.78 Seconds
(without alignments)
652.674 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543

Sequence: 1 MTEGALSFADFLAGIAAA.....LRGMAFVLVYDELKKVI 298

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	298	1 S03894	ADP, ATP carrier pr
2	1512	98.0	298	2 B43646	ADP, ATP carrier pr
3	1454	94.2	298	1 A29132	ADP, ATP carrier pr
4	1424	92.3	298	1 T60173	adenine nucleotide
5	1422	92.2	298	1 XMB0	ADP, ATP carrier pr
6	1418	91.9	298	1 S37210	ADP, ATP carrier pr
7	1409	91.3	298	1 A44778	ADP, ATP carrier pr
8	1405	91.1	298	2 S31814	ADP, ATP carrier pr
9	1184	76.7	301	1 S31935	ADP, ATP carrier pr
10	1041	67.5	313	2 T23207	hypothetical prote
11	1039	67.3	313	2 T25850	hypothetical prote
12	1038	67.3	300	2 T25371	hypothetical prote
13	993.5	64.4	300	2 T15206	hypothetical prote
14	978	63.4	339	2 A41677	ADP, ATP carrier pr
15	943	61.1	301	2 S51132	ADP, ATP carrier pr
16	778.5	50.5	307	2 A36582	ADP, ATP carrier pr
17	772	50.0	308	1 S30259	ADP, ATP carrier pr
18	769	49.8	322	2 T40526	adp/atp translocas
19	768	49.8	386	2 T09709	ADP, ATP carrier pr
20	766	49.6	313	1 XWNC	ADP, ATP carrier pr
21	764	49.5	326	2 T25728	hypothetical prote
22	762.5	49.4	305	2 S68154	ADP, ATP carrier pr
23	760.5	49.3	318	1 A31978	ADP, ATP carrier pr
24	756.5	49.0	306	2 T20012	hypothetical prote
25	750	48.6	387	2 S14876	ADP, ATP carrier pr
26	748	48.5	386	2 S21974	ADP, ATP carrier pr
27	747	48.4	306	2 T42011	ADP, ATP carrier pr
28	747	48.4	386	2 S17917	ADP, ATP carrier pr
29	744	48.2	387	2 S16568	ADP, ATP carrier pr

30	743	48.2	379	2 T04608	ADP, ATP carrier pr
31	742.5	48.1	385	1 S29852	ADP, ATP carrier pr
32	742	48.1	382	2 S33630	ADP, ATP carrier pr
33	739.5	47.9	386	2 S14874	ADP, ATP carrier pr
34	737.5	47.8	309	2 A24849	ADP, ATP carrier pr
35	734.5	47.6	379	2 S21313	ADP, ATP carrier pr
36	681.5	44.2	298	2 T24029	hypothetical prote
37	520.5	33.7	327	2 T51577	ADP, ATP translocas
38	393	24.8	325	2 T04273	hypothetical prote
39	381	24.7	352	2 T01729	hypothetical prote
40	372	24.1	358	2 T45934	hypothetical prote
41	370.5	24.0	415	2 T48171	hypothetical prote
42	369.5	23.9	381	2 T51158	hypothetical prote
43	368	23.8	475	2 T50686	peroxisomal Ca-dep
44	363	23.5	348	2 D84798	probable mitochond
45	344.5	22.3	332	2 T47703	Ca-dependent solut

ALIGNMENTS

```
RESULT
1
S03894
ADP, ATP carrier protein T3 - human
N:Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP,
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #ext_change 17-Mar-2000
C:Accession: S03894; B28116
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89236396
A:Accession: S03894
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Houldsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845
A:Accession: B28116
A:Molecule type: mRNA
A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>
A:Cross-references: GB:J03592; NID:9339722; PIDN:AAA36750.1; PID:9339723
A:Experimental source: liver
C:Genes: GDB:ANT3; ANT3Y
A:Gene: GDB:ANT3; ANT3Y
A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP, ATP carrier protein repeat homology <MAY>
F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP>
F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match      100.0%  Score 1543;  DB 1;  Length 298;
Best Local Similarity 100.0%  Pred. No. 7.3e-129;
Matches 298;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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QY	1	MTEGALSFADFLAGIAAAISKTAVPIERVKILLDOVHASQIADADKQYGVDCIVR	60
DB	1	MTEGALSFADFLAGIAAAISKTAVPIERVKILLDOVHASQIADADKQYGVDCIVR	60
QY	61	IPKEQGLVSWRGNLANVIRPTQALNFAFKDKYKQIFGCVDKHTQFRYFAGNLASG	120
DB	61	IPKEQGLVSWRGNLANVIRPTQALNFAFKDKYKQIFGCVDKHTQFRYFAGNLASG	120
QY	121	GAAGATSLCFVYPLDFARTRLADAVGSGTEREFRGLGDLVKTTSKDGIRGLYQGSFVS	180
DB	121	GAAGATSLCFVYPLDFARTRLADAVGSGTEREFRGLGDLVKTTSKDGIRGLYQGSFVS	180

QY 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTAVTAVAGVSPFDVRRMM 240
 |||||||
 Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTAVTAVAGVSPFDVRRMM 240
 |||||||
 QY 241 QSGRGADIMYGTVDCKMKIRDEGKAFKFGAMSNVLRGGAFAVLVLYDELKVI 298
 |||||||
 Db 241 QSGRGADIMYGTVDCKMKIRDEGKAFKFGAMSNVLRGGAFAVLVLYDELKVI 298
 |||||||

RESULT 2

B43646.
 ADP/ATP carrier protein T2 - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.7%; Pred. No. 4e-126;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||||||
 Db 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||||||
 QY 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRKFAAGNLASG 120
 |||||||
 Db 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRKFAAGNLASG 120
 |||||||
 QY 121 GAAGATSLCFVPLDFARTRLADVGKSGTEREFGDCLVKTSDGIRGLYOGFSYS 180
 |||||||
 Db 121 GAAGATSLCFVPLDFARTRLADVGKSGTEREFGDCLVKTSDGIRGLYOGFSYS 180
 |||||||
 QY 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTAVTAVAGVSPFDVRRMM 240
 |||||||
 Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTAVTAVAGVSPFDVRRMM 240
 |||||||
 QY 241 QSGRGADIMYGTVDCKMKIRDEGKAFKFGAMSNVLRGGAFAVLVLYDELKVI 298
 |||||||
 Db 241 QSGRGADIMYGTVDCKMKIRDEGKAFKFGAMSNVLRGGAFAVLVLYDELKVI 298
 |||||||

RESULT 3

A29132
 ADP/ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132
 R:Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A:Reference number: A29132; MUID:87166056
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Widsworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A24197; MUID:88124845
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26
 A:Note: There may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 5.4e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||||||
 Db 1 MTEQAISEFKDPLAGGIAAISKTAVERKLLQVHASKQIADKQYGYDCIYR 60
 |||||||
 QY 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRKFAAGNLASG 120
 |||||||
 Db 61 IPKEGVLSFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKHTQWRKFAAGNLASG 120
 |||||||
 QY 121 GAAGATSLCFVPLDFARTRLADVGKSGTEREFGDCLVKTSDGIRGLYOGFSYS 180
 |||||||
 Db 121 GAAGATSLCFVPLDFARTRLADVGKSGTEREFGDCLVKTSDGIRGLYOGFSYS 180
 |||||||
 QY 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTAVTAVAGVSPFDVRRMM 240
 |||||||
 Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNTIIVSWMIAGTAVTAVAGVSPFDVRRMM 240
 |||||||
 QY 241 QSGRGADIMYGTVDCKMKIRDEGKAFKFGAMSNVLRGGAFAVLVLYDELK 296
 |||||||
 Db 241 QSGRGADIMYGTVDCKMKIRDEGKAFKFGAMSNVLRGGAFAVLVLYDELK 296
 |||||||

RESULT 4

160173
 adenine nucleotide translocator - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: 160173
 R:Shinozuka, Y.; Kamida, M.; Yamazaki, N.; Terada, H.
 Biochim. Biophys. Acta 1152, 192-196, 1993
 A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: 160173; MUID:94002161
 A:Accession: 160173
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA3842.1; PID:g400427
 C:Genetics:
 A:Gene: ant1
 A:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2.4e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

[illegible]

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RESULT      5
XMBIO
ADP,ATP carrier protein T1 - bovine
N:Alternate names: ADP/ATP translocase T1
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
C:Accession: A43646; A24822; A03181; A61343; S69369
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
A:Biochemistry 20, 866-873, 1989
A>Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A:Reference number: A43646; MUID:89229093
A:Accession: A43646
A:Molecule type: mRNA
A:Residues: 1-298 <POM>
A:Cross-references: GB:M24102; NID:g529414; PIDN:AAA30768.1; PID:g529415
R:Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Comm. 138, 850-857, 1986
A>Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A:Reference number: A24822; MUID:86295775
A:Accession: A24822
A:Molecule type: mRNA
A:Residues: 208-298 <RAS>
A:Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
R:Aquila, H.; Misra, D.; Eulitz, M.; Klingenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A>Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
A:Reference number: A03181; MUID:82186267
A:Accession: A03181
A:Molecule type: Protein
A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <AOU>
A>Note: residue 52 may be methyllysine
R:Babel, W.; Wächter, E.; Aquila, H.; Klingenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A>Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
A:Reference number: A61343; MUID:82046808
A:Accession: A61343
A:Molecule type: protein
A:Residues: 205-298 <BAB>
R:Oetmeier, W.; Masson, K.; Kalina, S.
R. Oetmeier, W.; Masson, K.; Kalina, S.
Eur. J. Biochem. 227, 730-733, 1995
A>Title: [(3)H]7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP/ATP
A:Reference number: S69369; MUID:95172058
A:Accession: S69369
A:Molecule type: protein
A:Residues: 49-63;154-168 <OET>
C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
C:Complex: homodimer
C:Function:
A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP generated
A>Note: located in the inner mitochondrial membrane
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

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C-Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochondrion
E:5-39/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F:52/Modified site: N6-methyllysine (Lys) #status predicted

[illegible]

RESULT 6

ADP/ATP carrier protein T1 - mouse
N.Alternate names: adenine nucleotide carrier
C.Species: Mus musculus (house mouse)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C.Accession: S37210
R.Laplace, C.; Costet, P.
submitted to the EMBL Data Library, September 1993
A.Reference number: S37210
A.Accession: S37210
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-298 <LAP>
A.Cross-references: EMBL:X74510; NTD:g402627; PIDD:CAA52616.1; PTD:g402628
C.Genetics:
A.Gene: ANCL1
C.Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C.Keywords: duplication; transmembrane protein
F/5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F/110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F/207-299/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match	91.98;	Score 1418;	DB 2;	Length 298;
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Best Local Similarity 88.9%; Pred. No. 8.1e-118;

Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

1 MEEQATSEAKDEI ACCCTAAATCKTAVABTEBVKI I IOVOHASKOTADADKVKCTVDCIYB 60

1 M1E2W1S1F1A1N1U1L1E1A1O1S1A1M1A1S1N1A1V1A1F1E1N1V1A1E1E1B1E1Q1V1Q1H1A1S1K1Q1I1A1H1A1D1A1Q1I1K1O1I1V1D1C1I1V1A1U1

b 1 MGDALSLKDFLAGGIAAAVSKTAVAPIERVKLLLOYOHASKOISAEKQYKGIIDCVR 60

61 IPKEQVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASG 120

61 IPKEQGLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLCGVDRHKQFWRYFAGNLASG 120

[illegible]

121 GAAAGH13LCFVIFPDLFAKIKLAAADVGNDSIGENEFKBLGDLCAKIK3DGIKGLIYGR3VS 180

121 GAAGATSLCEVYPLDFARTRLADYVGKSSOREFENGIGDCLTKIEKSPDGLKGLYOGFSVS 180

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Oy 181 VGGIIYRAAFVGYDTRAKGMLPDPKNTHTIVSWMIQCTVAVAGVSYPPDTVRRMM 240
Db 181 VGGIIYRAAFVGYDTRAKGMLPDPKNTHTIVSWMIQCTVAVAGVSYPPDTVRRMM 240
Oy 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKKVI 298
Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKKVI 298

RESULT 7
A:ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP/ATP translocase 1
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A44778; S03893; A39893; A28116
R:Li, K.; Warner, C.R.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, M.
J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: A44778; MUID:89340499
A:Accession: A44778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LTA>
A:Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP tr
A:Reference number: S03893; MUID:89236396
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Nackelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a leader
A:Reference number: A39891; MUID:88041149
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
R:Experimental source: clone pHMANT
R:Houldsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in a
A:Reference number: A94197; MUID:88124845
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOH>
A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA36751.1; PID:g339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP/ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.3%, Score 1409; DB 1; Length 298;
Best Local Similarity 88.3%; Pred. No. 5, 1e-117;
Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

Oy 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKOIAADKQYKGIYDCIVR 60
Db 1 MGDHMSFLKDFLAGGVAANAASKTAVAPIERVKLLQVQHSKOISAKQYKGIIDCVVR 60
Oy 61 IPKEGVSIFSRGNLANIYRFFPTQALNFAFDKKQKQIFLGVDKHTQFWRFAGNLASC 120

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Db 61 IPKEGVSIFSRGNLANIYRFFPTQALNFAFDKKQKQIFLGVDKHTQFWRFAGNLASC 120
Oy 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFGLDCLVTKTSKGIGLVGFSVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFGLDCLVTKTSKGIGLVGFSVS 180
Oy 181 VGGIIYRAAFVGYDTRAKGMLPDPKNTHTIVSWMIQCTVAVAGVSYPPDTVRRMM 240
Db 181 VGGIIYRAAFVGYDTRAKGMLPDPKNTHTIVSWMIQCTVAVAGVSYPPDTVRRMM 240
Oy 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKKVI 298
Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKKVI 298

RESULT 8
A:ATP carrier protein T2 - mouse
N:Alternate names: adenine nucleotide translocase
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C:Accession: S31814
R:Costet, P.; Laplace, C.
submitted to the EMBL Data Library, January 1993
A:Reference number: S31814
A:Accession: S31814
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <COS>
A:Cross-references: EMBL:X70847
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP>
F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.1%, Score 1405; DB 2; Length 298;
Best Local Similarity 89.2%; Pred. No. 1, 1e-116;
Matches 264; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

Oy 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKOIAADKQYKGIYDCIVR 60
Db 1 MTEQAISFAKDFLAGGIAAISTKAVAPIERVKLLQVQHSKOIAADKQYKGIIDCVVR 60
Oy 61 IPKEGVSIFSRGNLANIYRFFPTQALNFAFDKKQKQIFLGVDKHTQFWRFAGNLASC 120
Db 61 IPKEGVSIFSRGNLANIYRFFPTQALNFAFDKKQKQIFLGVDKHTQFWRFAGNLASC 120
Oy 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFGLDCLVTKTSKGIGLVGFSVS 180
Db 121 GAAGATSLCFYVPLDFARTRLAADVKGSGTEREFGLDCLVTKTSKGIGLVGFSVS 180
Oy 181 VGGIIYRAAFVGYDTRAKGMLPDPKNTHTIVSWMIQCTVAVAGVSYPPDTVRRMM 240
Db 181 VGGIIYRAAFVGYDTRAKGMLPDPKNTHTIVSWMIQCTVAVAGVSYPPDTVRRMM 240
Oy 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKKVI 296
Db 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRMGAFVLYLDELKKVI 296

RESULT 9
A:ATP carrier protein - African malaria mosquito
N:Alternate names: Anopheles gambiae (African malaria mosquito)
C:Species: Anopheles gambiae (African malaria mosquito)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S31935; S31936
R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
A:Reference number: S31935

```


A:Accession: S31935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BE>
A:Cross-references: EMBL:Z21814; EMBL:Z21815
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
E:7-101/Domain: ADP,ATP carrier protein repeat homology <ACPI>
E:112-204/Domain: ADP,ATP carrier protein repeat homology <ACI2>
E:209-300/Domain: ADP,ATP carrier protein repeat homology <ACI3>

	Query Match	Best Local Similarity	Score 1184:	DB 1:	Length 301:
	Matches 231:	Conservative 23:	Mismatches 44:	Indels 2:	Gaps 1:
			76.7%:		
			Pred. No. 3.9e-97:		
QY	1 MTEQA--ISFAKDLFAGISIAAAISTAVAPIERVKLLLOVQHASKOIALADKQYKGIIVDCI	58			
	1	MTKKADPYGFADKFLAGISIAAIVSTAAVPIERVKLLLOVQHASKOIALADKQYKGIIVDCI	60		
QY	59 VRIPEQGVFLSPWRCNLNVIRYPTQLNLFPAFKRYKQOIFLGVDKHTQPMRYFAGNLA	118			
	61 VRIPEQGVIGAFCCGNLNVIRYPTQLNLFPAFKRYKQOIFLGVDKHTQPMRYFELGNLG	120			
QY	119 SGGAAATSLCEVYPLDFARTRLAADVCGKSTEREPRGLDCLVKTYSDDIRGLYQGS	178			
	121 SGGAAATSLCEVYPLDFARTRLADGVPGADGERFENGLDCLKTIVKSDGIIIGLYRGEN	180			
QY	179 VSVQGIILIIYRAAYFEGVYPTAKGLDPPKNTHTIVVSMIMQVTTAAVGAIVSYFEDVRRRM	238			
	181 VSVQGIILIIYRAAYFEGVYPTAKGLDPPKNTHTIVVSMIMQVTTAAVGAIVSYFEDVRRRM	240			
QY	239 MMSGRKADIMYTITVDCMKRIIFDEDEGKAFKFGKMSVVLNGMGAFVVLVLDLKKYI	298			
	241 MMSGRKADIMYTITVDCMKRIIFDEDEGKAFKFGKMSVVLNGMGAFVVLVLDLKKYI	300			

RESULT 10
T23207
hypothetical protein K01H12.2 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207
R:McMurray, A.
submitted to the EMBL Data Library, December 1995
A:Reference number: Z19707
A:Accession: T23207
A:Status: preliminary; translated from GR/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-313 <WIL>
A:Cross-references: EMBL:Z66218; PDB:1CAM; GSPDB:GN00022; CESP:K01H12.2
C:Experimental source: clone K01H12
C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A:Introns: 4/1: 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

	Query Match	67.5%	Score 1041:	D8 2;	Length 313;
	Best Local Similarity	70.9%;	Pred. No. 1.8e-84;		
	Matches 207; Conservative	29;	Mismatches 52;	Indels 4;	Gaps 3.
Oy	8 FAKDLAGGIAAISKTVAPIERKLLLOYOHASKQIADADYKGYIVCIIRPEKGV	67			
	: :				
Dd	25 FLIDLASGGTAAAVSKTAAPLERKLLLOYDASLTJTAADRKYGIYVLVRPKEDDY	84			
Oy	68 LSFMRGNLANVRYRPTOLNFAFKDKYKOIFLGGVDKHFORMRPFAGNLASGSAAAGTS	127			
	:				
Dd	85 AALWNGNLANVRYRPTOLNFAFDYTKNIIFOKGDKRKDWKFEPFAGNLASGSAAAGTS	144			
Oy	128 LCFVPLDFARTRLAADYGKSTGEREFLGDCLVKITFSDGIRGLIYGFSEVSYGIIITY	187			

Db 145 LCIVYPLDFANTRLIADVGKA - NREERKGLADCLVYLAKSDGPIGLRGFFVSVOGIIII 203

Qy 188 RAATGVGVDDTKGKML - DPKATITLVSMHIAQVYTAAGVSVSPDFVRRRRMMOSGRG 246

Db 204 RAATFGMDTKMVFYTAGKRLNFPAALAAIQVYTVSGIIISTPMDVRRRRMMOSGRK - 262

Qy 247 ADIMYGTVDWCRRKIFRDEGKAFPFKGAMSVNLKMGCAFLVLYDELKRVY 298

Db 263 - DVLTKNPLDCAVRIIKKEGMSAIFKGLSVNFGSTGGAFLVLAIVYDIQFI 313

```

RESULT 11
T25850
hypothetical protein T01B11.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25850
R:Geisels, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid T01B11.
A:Reference number: Z20099
A:Accession: T25850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-313 <GEI>
A:Cross-references: EMBL:U80931; PIDN:AA838001.1; GSPDB:GNO0022; CESP:T01B11.4
A:Experimental source: strain Bristol N2; clone T01B11
C:Genetics:
A:Gene: CESP:T01B11.4
A:Map position: 4
A:Insertion: 4/1, 191/2
C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology

```

Query Match	67.3%	Score 1039:	DB 2:	Length 313:			
Best Local Similarity	70.9%	Pred. NO.2.7e-84:					
Matches	207:	Conservative	29:	Mismatches 52: Indels 4: Gaps 3:			
Qy	8	EAKDFLAGGIAAISKTA	VAPIERVKLLLOVHASKQI	AAADKQYKGI	VDIVIRPEKGV	67	
Db	25	FLIDIASGGTAAAVSKTA	VAPIERVKLLLOVODASLT	JIAADRYKGI	VDIVIRPEKGV	84	
Qy	68	LSFMGKGLANVIRYRPT	OLNFAFDKYKQIPLGV	VDKHOTWRKFA	GNLASGGAAGTS	127	
Db	85	AALRMGKGLANVIRYRPT	OLNFAFDYTKNIFOK	GLDKKDPKRF	FAGNLASGGAAGTS	144	
Qy	128	LCFVYPLDFARTRLAD	YVSGSTGEREPKGLD	CLVYITKSDGI	RGLYOGFSV	VOGIIIT	187
Db	145	LCFVYPLDFARTRLAD	YVSGK-NEREKFG	LADCLVYITKSDP	IDLTYGFSV	VOGIIIT	203
Qy	188	RAAYFGVDTAKGML-P	DPKRNTHIVVSNM	IAOTVAAGVSY	PEPDYRRRM	MMOSGRK	246
Db	204	RAAYFGMDETAKMVE	TAAOSKRLFEFAA	MAIADVYVGS	ILSYPDYTR	RRRMMSGRK	262
Qy	247	ADIMTGTGVDCCRRK	IFRDEGKAFFK	GGANSVLRBM	GGAFVLYL	YDELKVI	298
Db	263	-DVLKKNLTDCAVKI	IKNEGMSAMK	GAISNVNRTG	GGALVLA	IDELDKFI	313

RESULT 12
T25371
hypothetical protein T27E9.1 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25371
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20024
A:Accession: T25371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <MIL>
A:Cross-references: EMBL:Z82059; PIDB:CA804874.1; GSPDB:GN00021; CESP:T27E9.1

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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:33:12 ; Search time 57.26 Seconds

(without alignments)
385.502 Million cell updates/sec

Title: US-09-393-441-33

Perfect score: 1543
Sequence: 1 MTEQAISEAFKDFLAGIAAA.....LRGKGAFVLVYDELKKVI 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq-1101:*

- 1: /SID58/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /SID58/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /SID58/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /SID58/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /SID58/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /SID58/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /SID58/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /SID58/gcgdata/geneseq/geneseq/AA1987.DAT.*
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- 11: /SID58/gcgdata/geneseq/geneseq/AA1990.DAT.*
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- 13: /SID58/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /SID58/gcgdata/geneseq/geneseq/AA1993.DAT.*
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- 20: /SID58/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /SID58/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /SID58/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1543	100.0	298	21	AAV71033	Human adenine nucl
2	1543	100.0	298	22	AAW39641	Human polypeptide
3	1543	100.0	298	22	AAU01200	Human adenine nucl
4	1543	100.0	323	22	AAW41427	Human polypeptide
5	1454	94.2	298	21	AAV71032	Human adenine nucl
6	1454	94.2	298	22	AAU01199	Human adenine nucl
7	1412	91.5	298	19	AAW61169	Anti protein. Mus
8	1385.5	89.8	297	21	AAV71031	Human adenine nucl
9	1385.5	89.8	297	22	AAU01198	Human adenine nucl
10	749.5	48.6	386	22	AAW00106	ADP/ATP carrier pr
11	742.5	48.1	346	21	AAW36577	Arabidopsis thalia

12	742.5	48.1	346	21	AAW37261	Arabidopsis thalia
13	742.5	48.1	346	21	AAW37264	Arabidopsis thalia
14	742.5	48.1	346	21	AAW38460	Arabidopsis thalia
15	742.5	48.1	363	21	AAW36576	Arabidopsis thalia
16	742.5	48.1	363	21	AAW37260	Arabidopsis thalia
17	742.5	48.1	363	21	AAW37263	Arabidopsis thalia
18	742.5	48.1	363	21	AAW38459	Arabidopsis thalia
19	742.5	48.1	381	21	AAW36575	Arabidopsis thalia
20	742.5	48.1	381	21	AAW37259	Arabidopsis thalia
21	742.5	48.1	381	21	AAW37262	Arabidopsis thalia
22	742.5	48.1	381	21	AAW38458	Arabidopsis thalia
23	742.5	48.1	992	21	AAW38672	Arabidopsis thalia
24	742.5	48.1	1009	21	AAW38671	Arabidopsis thalia
25	742.5	48.1	1027	21	AAW38670	Arabidopsis thalia
26	739.5	47.9	346	21	AAW17731	Arabidopsis thalia
27	739.5	47.9	363	21	AAW17730	Arabidopsis thalia
28	739.5	47.9	381	21	AAW17729	Arabidopsis thalia
29	689.5	44.7	330	21	AAW20658	Arabidopsis thalia
30	688.5	44.6	330	21	AAW39398	Arabidopsis thalia
31	679.5	44.0	333	21	AAW06857	Arabidopsis thalia
32	679.5	44.0	333	21	AAW06856	Arabidopsis thalia
33	679.5	44.0	368	21	AAW06855	Arabidopsis thalia
34	672	43.6	306	21	AAW12916	Arabidopsis thalia
35	672	43.6	306	21	AAW20659	Arabidopsis thalia
36	659.5	42.7	291	21	AAW20659	Arabidopsis thalia
37	658.5	42.7	291	21	AAW39399	Arabidopsis thalia
38	654	42.4	291	21	AAW12917	Arabidopsis thalia
39	654	42.4	291	21	AAW16975	Arabidopsis thalia
40	588.5	38.1	263	21	AAW12918	Arabidopsis thalia
41	588.5	38.1	263	21	AAW16976	Arabidopsis thalia
42	585.5	37.9	249	21	AAW20660	Arabidopsis thalia
43	584.5	37.9	249	21	AAW39400	Arabidopsis thalia
44	572.5	37.1	312	21	AAW28188	Arabidopsis thalia
45	563.5	36.5	228	21	AAW28189	Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAV71033	standard; Protein: 298 AA.
XX	XX
AC	AAV71033:
XX	XX
DT	29-AUG-2000 (first entry)
XX	XX
DE	Human adenine nucleotide translocator ANT3.
XX	XX
XX	Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotropic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparkinson; cerebroprotective; therapeutic; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; liver's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDP;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	XX
OS	Homo sapiens.
XX	XX
PN	W0200026370-A2.
XX	XX
PD	11-MAY-2000.
XX	XX
XX	03-NOV-1999; 99W0-US25883.
XX	XX
PR	03-NOV-1998; 98US-0185904.
XX	XX
PR	08-SEP-1999; 99US-0393441.
XX	XX
PA	(MITO-) MITOKOR.
XX	XX

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
PI Ghosh SS;
XX
XX WPI: 2000-365619/31.
DR N-PSDB: AAD00521.
XX
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease
XX
XX
PS Claim 46; Page 173-174; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.
XX
XX Sequence 298 AA:

Query Match 100.0%; Score 1543; DB 21; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVHASKQIADKQYGIYDCIVR 60
DB 1 mteqaisfakdfliaggiaaistavapiervkllqvhaaskqiaadkqygiydcivr 60
QY 61 IRKEGCVLSFMWGNLANVRYRFPPTQALNFAFDKXKQIRFGVDKHTQWRPFAGNLAGS 120
DB 61 ipkegcvlsfwmgnlanvryrftqalnfafdkyqirflgvdktqwrpfagnlasg 120
QY 121 GAAGATSLCFVYPLDFARTRLADVKGSGTEREFRGLDCLVKIRKSDSIRLQYGFVS 180
DB 121 gaagatslcfvypldfartrladvksgsterefrglvclvklksdgsrlqygfvs 180
QY 181 VGGIITIRRAAYGVYDTAKGMLPDKNTHIVVSWMAIQVTAVAGVSYRPFDTVRRRMM 240
DB 181 vggiiitrraaygyvdtakgmlpdknthiivswmiaqvtaavagvsyrfdtvrrmm 240
QY 241 QSGRKADIMYGTDCWKRIFRDEGKAFKFGAMSNVLRGAGAFVLVYDELKKVI 298
DB 241 qsgrrgadlmgytgcwkrifrdgkafkfgamsnvlrngagafvlvyldekkvi 298

RESULT 2
AAM39641
ID AAM39641 standard; Protein: 298 AA.

XX AAM39641;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2786.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW Leukaemia.
XX
XX Homo sapiens.
XX
XX WO200153312-A1.
XX
XX
PD 26-JUL-2001.
XX
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Dimaac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB: AA158797.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
PT
XX
XX Example 4; SEQ ID NO 2786; 10078pp; English.

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AA442213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localized neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed specification.
XX

Sequence 298 AA:

Query Match 100.0%; Score 1543; DB 22; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAIISFAKDFLAGGIAAISKTAAPIERVKLLQVHASKQIADKQYGIYDCIVR 60
DB 1 mteqaisfakdfliaggiaaistavapiervkllqvhaaskqiaadkqygiydcivr 60
QY 61 IRKEGCVLSFMWGNLANVRYRFPPTQALNFAFDKXKQIRFGVDKHTQWRPFAGNLAGS 120
DB 61 ipkegcvlsfwmgnlanvryrftqalnfafdkyqirflgvdktqwrpfagnlasg 120
QY 121 GAAGATSLCFVYPLDFARTRLADVKGSGTEREFRGLDCLVKIRKSDSIRLQYGFVS 180
DB 121 gaagatslcfvypldfartrladvksgsterefrglvclvklksdgsrlqygfvs 180
QY 181 VGGIITIRRAAYGVYDTAKGMLPDKNTHIVVSWMAIQVTAVAGVSYRPFDTVRRRMM 240
DB 181 vggiiitrraaygyvdtakgmlpdknthiivswmiaqvtaavagvsyrfdtvrrmm 240

QY 241 QSGRKADIMYTGTVDCKRKIFRDEGKAFKFGAMSNVLGMCAGFVLYLDELKRVY 298
 |||
 DB 241 qsgrrkgadlmtygtvdckwrkifrddegkafkfgawsnvlrgmgafvlyldelkrrv 298

RESULT 3

AAU01200

ID AAU01200 standard; Protein; 298 AA.

AC AAU01200;

DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-3 (ANT-3) protein.

KW Human; adenine nucleotide translocator-3; ANT-3; MPT; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN MO200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-US30535.

PR 03-NOV-1999; 99US-0434354.

PA (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frliger LG;

PI Velicelcebi G, Davis RE;

DR WPI: 2001-291054/30.

DR N-PSDB: AAS05903.

PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -

PS Disclosure: Fig 2; 186pp; English.

CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

SO Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 22; Length 298;

Best Local Similarity 100.0%; Pred. No. 2,5e-157;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEOAISFAKDFLAGIAAISTKTAVERKLLLOVGHASKOIADKQYKGIYDCTVR 60

DB |||
 1 mtegaistsfakdfliagsglaaaisktavapiervklllvqbnaskqiaadkqygiydvctivr 60
 QY 61 IPKEGCVLSFWRGNLANVIRFPTQALNFAFKDKYKOIFLGVDKHTQFRRFRAGNLASG 120
 |||
 DB 61 ipkegcvlsfwrnlanvlyrfptqalnfafkdkykgiflgyvdkhtqfwrfragnlasg 120
 QY 121 GAAGATSLCFVYPLDFARTPLADVCGSKGEREPRGIGDCLVIRITSDDGIRGLYOGFSVS 180
 |||
 DB 121 gaagatslcfvypldfartpladvgksgerereprgigdcivrlksdglrlyqgisvs 180
 QY 181 VGGIIIVRAAYFGVYDPAKGMPLDPKNTHTVSMIAQVTAAGVVSYPFDVRRRMM 240
 |||
 DB 181 vggilivraayfgvydtkgmpldpknthtvsmiaqvtaagvvsypfdvrrrrmm 240
 QY 241 QSGRKADIMYTGTVDCKRKIFRDEGKAFKFGAMSNVLGMCAGFVLYLDELKRVY 298
 |||
 DB 241 qsgrrkgadlmtygtvdckwrkifrddegkafkfgawsnvlrgmgafvlyldelkrrv 298

RESULT 4

AAM41427

ID AAM41427 standard; Protein; 323 AA.

AC AAM41427;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6358.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; hemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW Leukemia.

OS Homo sapiens.

PN MO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000MO-US34263.

PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.

PA (HYSE-) HYSEQ INC.

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

DR WPI: 2001-442253/47.

DR N-PSDB: AA160583.

PT Novel nucleic acids and polypeptides, useful for treating disorders

CC such as central nervous system injuries -

CC Example 2; SEQ ID NO 6358; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

CC
 XX Sequence 323 AA;

Query Match 100.0%; Score 1543; DB 22; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2,8e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASQIADKQYKGIYDCIVR 60
 DB |||||||
 QY 26 mteqaisfakdfliaggiaaistkavapiervklllvqghaskqladkqykvldcivr 85
 DB |||||||
 QY 61 IRKEGCVLSFMGNGLANVRYRFPQTALNFAFDKKYQIFLGVDKHTQFWRFAAGNLASG 120
 DB |||||||
 QY 86 lpekegvslfwrnglanvlyrlpqalnfafkdkyqiflgvdkhtqfwrfaagnlasg 145
 DB |||||||
 QY 121 GAAGATSLCFVYPLDFARLADYKSGSTEREFGIDCLVKITKSDIRLQYGFYSV 180
 DB |||||||
 QY 146 gaagatslcfvypldfarladyksgsterefgrlgdclvkiktsdgrlqygfysv 205
 DB |||||||
 QY 181 VOGIITIRRAHYGVYDTAKGMLPDKNTHIVSWMIAQTVTAAGVSYPEDTVRRRMM 240
 DB |||||||
 QY 206 vgiitirrahygvdytackgmldpdknthiivswmiaqtvtaagvsypedtvrrmm 265
 DB |||||||
 QY 241 GSGRGADIMYGTDCWKIRFDEGKAFKFGAMSNVIRGSGAFVLYLYDELKKVI 298
 DB |||||||
 QY 266 gsgrgadimygtdcwkirfdegkafkfgamsnvirgsgafvlylydelkkvi 323

RESULT 5
 AAY71032
 ID AAY71032 standard; Protein: 298 AA.

XX
 AC AAY71032;

XX
 DT 29-AUG-2000 (first entry)

XX
 DE Human adenine nucleotide translocator ANT2.

XX
 KM Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KM mitochondrial permeability transition; neuroprotective; nootropic;
 KM antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KM antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.

XX
 OS Homo sapiens.

XX
 PN WO200026370-A2.

XX
 PD 11-MAY-2000.

XX
 PF 03-NOV-1999; 99WO-US25883.

XX
 PR 03-NOV-1998; 98US-0185904.

XX
 PR 08-SEP-1999; 99US-0393441.

XX
 PR (MITO-) MITOKOR.

XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo FR;
 PI Ghosh SS;

XX
 DR WPI: 2000-365619/31.

XX
 DR N-PSDB: AAD00520.

XX
 PR Recombinant construct encoding adenine nucleotide translocator
 PR polypeptide, useful e.g. in screening for potential therapeutic agents
 PR against mitochondrial disease

XX
 PS Claim 45; Page 172-173; 175pp; English.

XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.

XX
 SQ Sequence 298 AA;

Query Match 94.2%; Score 1454; DB 21; Length 298;
 Best Local Similarity 92.6%; Pred. No. 8.9e-148;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAAPIERVKLLQVQHASQIADKQYKGIYDCIVR 60
 DB ||:|||||
 QY 1 mteqaisfakdfliaggiaaistkavapiervklllvqghaskqladkqykvldcivr 60
 DB ||:|||||

QY 61 IRKEGCVLSFMGNGLANVRYRFPQTALNFAFDKKYQIFLGVDKHTQFWRFAAGNLASG 120
 DB |||||

QY 61 lpekegvslfwrnglanvlyrlpqalnfafkdkyqiflgvdkhtqfwrfaagnlasg 120
 DB |||||

QY 121 GAAGATSLCFVYPLDFARLADYKSGSTEREFGIDCLVKITKSDIRLQYGFYSV 180
 DB |||||||

QY 121 gaagatslcfvypldfarladyksgsterefgrlgdclvkiktsdgrlqygfysv 180
 DB |||||||

QY 181 VOGIITIRRAHYGVYDTAKGMLPDKNTHIVSWMIAQTVTAAGVSYPEDTVRRRMM 240
 DB |||||||

QY 181 vgiitirrahygvdytackgmldpdknthiivswmiaqtvtaagvsypedtvrrmm 240
 DB |||||||

QY 241 GSGRGADIMYGTDCWKIRFDEGKAFKFGAMSNVIRGSGAFVLYLYDELKKVI 296
 DB |||||||

QY 241 gsgrgadimygtdcwkirfdegkafkfgamsnvirgsgafvlylydelkkvi 296
 DB |||||||

XX
 RESULT 6

XX
 ID AAU01199 standard; Protein: 298 AA.

XX
 AC AAU01199;

XX
 DT 07-SEP-2001 (first entry)

XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.

XX
 KM Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

DB 121 gaagatslcfvypldfarttlaadvkgsqrefngldcltklfksdglklygfsvs 180
 QY 181 VGGIIRRAAFGVYDTAKGMLPDPKNTIHVSWMIAGTVTAAGVSYFPDTRRRMM 240
 DB 181 vggiliryraayfgvydtaqgmldpdknvhlfvswmlagstvavgllyspfdtvtrrmm 240
 QY 241 GSGRKADIMYGTVDCKMKIRDEGKAFKFGAMSNIIRGKGAFVLYVDELKVI 298
 DB 241 gsgrkadimygvtcdwkrfkakdeganaefkfgawsnvirgmgaftvlyvdeikkyv 298

RESULT 8
 AAY71031
 ID AAY71031 standard; Protein: 297 AA.
 AC AAY71031;
 DT 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator ANT1.
 XX
 KM Human: adenine nucleotide translocator: ANT1; mitochondria: ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KM mitochondrial permeability transition; neuroprotective; neurotropic;
 KM antiParkinsonian: cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KM antiparkinsonian: cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 XX
 OS Homo sapiens.
 XX WO200026370-A2.
 XX PD 11-MAY-2000.
 XX PF 03-NOV-1999; 99WO-US25883.
 XX PR 03-NOV-1998; 98US-0185904.
 XX PR 08-SEP-1999; 99US-0393441.
 XX PA (MITO-) MITOKOR.
 XX PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR MPI: 2000-365619/31.
 DR N-PSDB: AAD00519.
 XX PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 44; Page 172; 175pp; English.

The patent discloses a method to produce adenine nucleotide translocator
 (ANT) proteins or ANT fusion proteins using recombinant expression
 constructs. ANT is a nuclear encoded protein and a major component of
 inner mitochondrial membrane. It mediates transport of adenosine
 di/tri-phosphates across the mitochondrial inner membrane and also serves
 as an important molecular component of the mitochondrial permeability
 transition pore, a modulator of apoptosis. ANT is used to identify agents
 or ligands that bind to, or interact with it. The ANT ligands are used to
 detect or isolate ANT in a biological sample, and therapeutically for
 regulating mitochondrial pore activity, for treating diseases associated
 with altered mitochondrial function, including Alzheimer's, Parkinson's
 and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 epilepsy red ragged fibre syndrome. The present sequence is an

CC adenine nucleotide translocator ANT1 from human brain.
 XX
 SQ Sequence 297 AA;
 Query Match 89.8%; Score 1385.5; DB 21; Length 297;
 Best Local Similarity 87.2%; Pred. No. 2e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEOATSPAKDFLAGIAAISKTAAPERVKLLLOVHASKOIAADQYKIVDCIAR 60
 DB 1 mgdhawslfkdfilaagavaavsktavaplerklllqvgnaskqisaekyqgllidcvrr 60
 QY 61 IPEQGVLSFMRGNLANVIRYFPTQALNFAFKDKYKQIFLGVGDKRHTQFMRFAAGNLASG 120
 DB 61 lpekgvflsfmrgnlanviryfpqtalnfafkdkyqlflgvdvdkhqwrfaglnaag 120
 QY 121 GAAGATSLCFVYPDPFARKRLAADVCKSTEREKFGCLVKTIRKSDGIRLQYGFVS 180
 DB 121 gaagatslcfvypdpfarkrlaadvcksterefngldcltklfksdglrlygqfvs 179
 QY 181 VGGIIRRAAFGVYDTAKGMLPDPKNTIHVSWMIAGTVTAAGVSYFPDTRRRMM 240
 DB 180 vggiliryraayfgvydtaqgmldpdknvhlfvswmlagstvavgllyspfdtvtrrmm 239
 QY 241 GSGRKADIMYGTVDCKMKIRDEGKAFKFGAMSNIIRGKGAFVLYVDELKVI 298
 DB 240 gsgrkadimygvtcdwkrfkakdegakafkfgawsnvirgmgaftvlyvdeikkyv 297

RESULT 9
 AAU01198
 ID AAU01198 standard; Protein: 297 AA.
 AC AAU01198;
 DT 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX
 KM Human: adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX WO200132876-A2.
 XX PD 10-MAY-2001.
 XX PF 03-NOV-2000; 2000WO-US30535.
 XX PR 03-NOV-1999; 99US-0434354.
 XX PA (MITO-) MITOKOR.
 XX PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelebi G, Davis RE;
 DR MPI: 2001-291054/30.
 DR N-PSDB: AAS05901.
 XX PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure: Fig 2; 186pp; English.
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MTP) pore components responsible for mediating transport

SQ Sequence 297 AA;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1.

Db 1 mgdhawslkdf lagavaavstapiervk11lqvghaskqisaekykgildcvr 60

Db 61 lpkeggflsfwrgnlanviryfptgalnfafkdkkykqlflgvdrrhkqfwryfagnlasg 1200

Db 121 gaagatslcfvpldfatr laadvgr-aqrefhlgdcilikifksdglrglyggnvs 179

Db 180 vqglllyraayfgvydtakgmlpdpknvhi fvs wmiagsvtavagllsy pfdt vrrmm 239

Db 240 qsgtgrgadlmytgtvtvdcwrlakdegakafkgaawnlrgmgafvlvlyde::kkyv 297

RESULT 10

ID AAM00106 standard; Protein; 386 AA.

AC AAM001.06;

DT 28-SEP-2001 (first entry)

DE ADP/ATP carrier protein sequence #1774.

KW Moss; carbohydrate metabolism related protein; CMRP; sugar; cofactor;

XX XX

OS Physcomitrella patens.

PN WO200144476-A2.

PD 21-JUN-2001

PF 14-DEC-2000; 2000WO-EP12697.

PR 16-DEC-1999; 99US-0171101.

PA (BADI) BASF PLANT SCI GMBH.

PI Lerchl J, Renz A, Ehrhardt T, Reindl A, Cirpus P, Bischoff F;

PI Frank M, Freund A, Duwenig E, Schmidt R, Reski R;

XX

DR N-PSDB; AAH88792.

DR N-PSDB; AAH88792.

PT Novel moss nucleic acid molecules encoding a carbohydrate metabolism

PT as carbohydrates, cofactors and enzymes from microorganisms and plants

PS Claim 30; Page 131; 133pp; English.

CC are used in the sequencing of the CMPD cDNA sequences of the invention.

SQ Sequence 386 AA;

Matches 157; Conservative 44; Mismatches 84; Indels 9; Gaps 5.

[illegible]

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QY 126 TSLCFVPLDFARTRLADV---GKSGTEREFGGLGDCLVKITKSDGIRGLYQGFSSVQ 182

QY 183 GIIYRAYEGVYDTAKG-MLPDPKNTTHIVSWMIAQTVTAVAGVSYPEDTVRRMMQ 241

QY 242 SGRKGADIMYTGTVDCWRK.IFRDEGGKAFKGAWSNVL RGMGAFVLVLYDELK 295

Db 323 sgea---vkynsgmdafkqllakegaksllfkagaganllravagavlsgydqlq 373

RESULT 11

ID AAG36577 standard; protein; 346 AA

AC AAG36577;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 44845.

KW Protein identification; signal transduction pathway; metabolic pathway;

KW termination sequence.

XX
X

XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-011825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132486.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
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Query Match 48.1% Score 742.5; DB 21; Length 346;
Best Local Similarity 52.8% Pred. No. 2,7e-71;
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DB 102 degfsglwrntanvlyfptqalnfaIkdyfkrllnfkxdr-dgykwkwaagnlaasgaa 160
QY 124 GATSLCFVYLDPAFRTIAD---VCKSGTEREFRCIGDCLVKTITKSDGIRGLYOGFSVS 180
DB 161 gassllfyvldyartclandakaakkgygrfdgldvdyrtkltkdglaglyrgrlnis 220
QY 181 VGGIIIRAAVFCVYDTAK-----GMLPDPKNTIIVSMMIAQTVTAAGVSTYPTDTR 235
DB 221 cvglIvryrlyfglydsdvkpvlltgdIdqdsffasfaIgwI---tnaglasypIdtvr 276
QY 236 RRMNMOSGRGALIMTGTVDCKRKIFRDGGAFFGKAANSNVLRGGAFAVLVLYDELK 295
DB 277 rrmnmssgae---vkysidaikqllknegakslfkagaganllravagavlsqydklq 333
QY 296 KVI 298
DB 334 IIV 336

RESULT 12
AAG37261

ID AAG37261 standard; Protein; 346 AA.
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AC 18-OCT-2000 (first entry)
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45788.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999: 99US-0121825.
PR 05-MAR-1999: 99US-0123180.
PR 09-MAR-1999: 99US-0123548.
PR 23-MAR-1999: 99US-0125788.
PR 25-MAR-1999: 99US-0126264.
PR 29-MAR-1999: 99US-0126785.
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PR 16-APR-1999: 99US-0129845.
PR 19-APR-1999: 99US-0130077.
PR 21-APR-1999: 99US-0130449.
PR 23-APR-1999: 99US-0130510.
PR 23-APR-1999: 99US-0130891.
PR 28-APR-1999: 99US-0131449.
PR 30-APR-1999: 99US-0132048.
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PR 04-MAY-1999: 99US-0132484.
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PR 06-MAY-1999: 99US-0132486.
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RESULT 13
AAG37264
ID AAG37264 standard; Protein: 346 AA.
XX AAG37264;
AC
XX 18-OCR-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 45792.
DE
XX
KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
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PR 28-OCT-1999; 99US-0161920.
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PR 29-OCT-1999; 99US-0162142.

Query Match 48.1%; Score 742.5; DB 21; Length 346;
Best Local Similarity 52.8%; Pred. No. 2.7e-71;
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Db 102 deqfsgslwrgntanvrlfptqelnfafrkrlfnfkfddr-dgywkwfaagnlasgaa 160
QY 124 GATSLCFVYPLDFARTRLAD---VGKSGTEREFGDLGDLVKTITSDSIRGLYOGFSVS 180
Db 161 gaeellfvyssldyartrellandakaakggggrqfdglvdvyr-ktkltdglaglyrgfnls 220
QY 181 VCGIITRYRAAYFGVDTAK-----GMLPDKNTNHYVSMIAQTVAYAGVVSYPEDTVR 235
Db 221 cvglIvYrglyfIygsavprvlltqdlqdsffasfaIgwvl----lmgaslasypldtvr 276
QY 236 RRMAMOSGRKGADIMYTGVDICWRKIFREBGGKAFPKGAMSNVLRMGGAFLVLYDELK 295
Db 277 rrrmmmtsgea---vkysldatfkqllknegakslfksgaganlltravagaylsgydkIq 333
QY 296 KVI 298
Db 334 lIv 336

RESULT 14
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ID AAG38460 standard; Protein; 346 AA.
XX
AC AAG38460;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47451.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 05-FEB-1999; 99US-0121825.
PR 09-MAR-1999; 99US-0123180.
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PR 25-MAR-1999; 99US-0125788.
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PR 06-APR-1999; 99US-0127462.
PR 08-APR-1999; 99US-0128234.
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Query Match 48.1%; Score 742.5; DB 21; Length 346;
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Db 102 deqfsglwzgnfanvlyrptqalnfaIdfkyfkrllnfkdr-dgykwkfaqnlasgaa 160
QY 124 GATSLCEVYPLDFARTRLAD--VGKSGTEREFRGLDCLVKTIKSDIRGLYGFVS 180
Db 161 gasallfyvslgyarclandakaakkggrgfdglvdvyrkkltdglaglyrgfnls 220
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Db 221 cvgllyvrygllyglvsvkprvlltqldqsfasfalgvli---tngaglaspyldtvy 276
QY 236 RMMNMGSGKAGADIMYTGVCWRKIFRDEGGAFFKAGMSNVLRGMGAFVLVDELK 295
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX Arabidopsis thaliana.
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PD 06-SEP-2000.
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Query Match 48.1%; Score 742.5; DB 21; Length 363;
Best Local Similarity 52.8%; Pred. No. 2,8e-71;
Matches 160; Conservative 45; Mismatches 77; Indels 21; Gaps 7;

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OY 296 KVI 298
DB 351 IIV 353

Search completed: February 13, 2002, 09:33:13
Job time: 110 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 : Search time 55.37 Seconds
(without alignments)
784.592 Million cell updates/sec

Title: US-09-393-441-31
Perfect score: 1553
Sequence: 1 MGDHWSFLKDFLAGAVAA.....LRGGAFLVLVDKIKYV 297

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP_invertebrate: *
6: SP_mammal: *
7: SP_mhc: *
8: SP_organelle: *
9: SP_phage: *
10: SP_plant: *
11: SP_rodent: *
12: SP_virus: *
13: SP Vertebrate: *
14: SP_unclassified: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1463.5	94.2	298	11	062164 mus musculu
3	1377.5	88.7	298	13	09YTIC4 Oryctolagus
4	1377.5	88.7	298	13	09PRH1 Oryctolagus
5	1374.5	88.5	298	13	09PRH2 Oryctolagus
6	1366.5	88.0	298	13	0919M9 Oryctolagus
7	1241.5	79.9	300	5	09NHWS Oryctolagus
8	1234.5	79.5	317	13	091336 Oryctolagus
9	1183	76.2	288	5	044093 Oryctolagus
10	1183	76.2	288	5	044094 Oryctolagus
11	1147	73.9	307	5	062526 Oryctolagus
12	1139.5	73.4	304	5	025129 Oryctolagus
13	1101.5	70.9	315	4	09HOC2 Oryctolagus
14	1045.5	67.3	313	5	091410 Oryctolagus
15	1043.5	67.2	313	5	021103 Oryctolagus
16	1037.5	66.8	300	5	045865 Oryctolagus
17	1005.5	64.7	300	5	001813 Oryctolagus
18	993.5	64.0	300	5	017407 Oryctolagus
19	989.5	63.7	309	5	097470 Oryctolagus

20	959	61.8	307	8	09XM22 Oryctolagus
21	950	61.2	318	5	09B136 Oryctolagus
22	905.5	58.3	301	5	025692 Oryctolagus
23	904.5	58.2	301	5	026006 Oryctolagus
24	841.5	54.2	170	6	09XS69 Oryctolagus
25	772	49.7	306	5	018683 Oryctolagus
26	757.5	48.8	305	3	09P8M1 Oryctolagus
27	750.5	48.3	307	5	076286 Oryctolagus
28	748.5	48.2	303	3	074260 Oryctolagus
29	746.5	48.1	379	10	049447 Oryctolagus
30	745.5	48.0	326	5	091270 Oryctolagus
31	743.5	47.9	307	5	026697 Oryctolagus
32	740.5	47.7	386	10	093767 Oryctolagus
33	738.5	47.6	388	10	049875 Oryctolagus
34	731.5	47.1	317	5	09N647 Oryctolagus
35	731	47.1	385	10	09P152 Oryctolagus
36	728.5	46.9	306	3	078754 Oryctolagus
37	727.5	46.8	331	10	041628 Oryctolagus
38	708	45.6	305	3	09P876 Oryctolagus
39	705	45.4	305	3	09P875 Oryctolagus
40	681	43.9	330	10	09PM86 Oryctolagus
41	676	43.5	298	5	021809 Oryctolagus
42	659	42.4	262	10	09AVT6 Oryctolagus
43	508	32.7	327	10	09LF44 Oryctolagus
44	486	31.3	162	5	026130 Oryctolagus
45	461	29.7	158	5	076467 Oryctolagus

ALIGNMENTS

RESULT 1
ID 046373 PRELIMINARY: PRT, 298 AA.
AC 046373:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKLETRAL MUSCLE;
RA Yamaguchi N., Kasai M.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -!- INNER MEMBRANE (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB009386; BAA23777.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; Mitoc_carf. 3.
DR PRINTS: PS00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA: 32901 MW: CAFA32C8B164AD78 CMC64;

Query Match 94.3%: Score 1464.5; DB 6; Length 298;
Best Local Similarity 94.6%: Pred. No. 1.2e-126;
Matches 282; Conservative 7; Mismatches 8; Indels 1; Gaps 1;
OY 1 MGDHWSFLKDFLAGAVAAVKTAAPLRYKLLLOVQHASKOISAEKQYGIIDCYVR 60
DB 1 MSQDLSFLKDFLAGVAAVSKTAAPLRYKLLLOVQHASKOISAEKQYGIIDCYVR 60
OY 61 IREKGFSLFNGNLANVIRYPTQALNFAFKDKQFLGVDNRHKKQFWRFAAGNLASG 120
DB 61 IREKGFSLFNGNLANVIRYPTQALNFAFKDKQFLGVDNRHKKQFWRFAAGNLASG 120

QY	121	GAAATSTSCFEYPLDPAFRTLADYGR - RAOREFHGLGCIIRKFSQDRLGXYGFNVS	179
	121		179
Db	121	GAAATSTSCFEYPLDPAFRTLADYGVKGAQAQRFESGLGCKIRKFSQDRLGXYGFNVS	180
	180	VQIIITIRAAVFGYVDTAKMGLDPDKNVHLEYSWMAIQAQSVTAAGLSYFPDVTRRMM	239
QY	240	OSGRKGDIMYTGVCDCWKRIANDDEGAKAFKFKAMSNVLRKGGAFVLYVDEIKKY	297
	240		297
Db	241	OSGRKGDIMYTGVCDCWKRIANDDEGAKAFKFKAMSNVLRKGGAFVLYVDEIKKY	298
	241		298
RESULT	2		
ID	062164	PRELIMINARY; PRT; 298 AA.	
AC	062164;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DE	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)		
DE	ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1) (SIMILAR		
DE	TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE		
DE	TRANSLOCATOR), MEMBER 4.)		
GN	SLOC25A4 OR MANCI OR ANTI1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_Taxid:10090;		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-BALB/C; TISSUE=MUSCLE;		
RA	Laplace C., Costet P.;		
RL	Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Ievy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;		
RT	"Expression and Sequence analysis of the mouse adenine nucleotide		
RT	translocase 1 and 2 genes."		
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RA	Strausberg R.;		
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL		
CC	INNER MEMBRANE (BY SIMILARITY).		
CC	-1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.		
DR	EMBL: X74510; CAAS2616.1; -		
DR	EMBL: AF240002; AAF64470.1; -		
DR	EMBL: BC003791; AAH03791.1; -		
DR	MGI: MGI:1353495; SLOC254.		
DR	InterPro: IPR001993; MitochCarrier.		
DR	InterPro: IPR002067; MLCCarrier.		
DR	Pfam: PF00153; mito_carrt.3.		
DR	PRINTS: PR00926; MITOCARRIER.		
DR	PROSITE: PS00215; MITOCH_CARRIER.3.		
KM	Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.		
QZ	SEQUENCE 298 AA; 32904 MW; 3AB49FEAB0981462 CRC64;		

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Query Match          94.2%  Score 1463.5  DB 11  Length 298;
Best Local Similarity 94.0%  Pred. No. 1.5e-126;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

OY  1  MGDHMSFLKDPDLAAGVAAAVSKTVAPIERKLLLOVHASKQISAEKYOYGIIDCVRR 60
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  1  MGDQSLSTLKDPLAGGIAAAVSKTVAPIERKLLLOVHASKQISAEKYOYGIIDCVRR 60

OY  61  IPKEGGFSFWMGNLANIYRFPQALNFAFDKXKQLELGVGDHDKHQRWRFAGNLASG 120
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  61  IPKEGGFSFWMGNLANIYRFPQALNFAFDKXKQIFLGVGDHDKHQRWRFAGNLASG 120

OY  121  GAAGATSLCFVYPLDFAFTRLADYGR-RAQREPHGLGCCIIRKRSQSLRGLYGFNVS 179
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

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Db	121	GAGATSTLCEFYVPLDEAFRTRLADVDKSSQREFNLGDLCTIKFSDBLKLKLYGFFSVS	180
Qy	180	VQGIITIRAAVFEGYDPAKAKMLDPDPKNVHIFVSMVLAQSYTAVAGLSTPEDTVRRMM	239
Db	181	VQGIITIRAAVFEGYDPAKAKMLDPDPKNVHIFVSMVLAQSYTAVAGLSTPEDTVRRMM	240
Qy	240	QSGKKAGDIWYGTVDWRRIARDEGAKAFKSGAMSNVLRGMAFVLVYDEIKRYV	297
Db	241	QSGKKAGDIWYGTVDWRRIARDEGAKAFKSGAMSNVLRGMAFVLVYDEIKRYV	298
RESULT	3		
QYVIC4	QYVIC4	PRELIMINARY;	PRT; 298 AA.
AC	QYVIC4		
DT	01-MAY-1999	(TEMBLrel. 10, Created)	
DT	01-MAY-1999	(TEMBLrel. 10, Last sequence update)	
DT	01-JUN-2001	(TEMBLrel. 17, Last annotation update)	
DE	ADP/ATP TRANSLOCASE.		
OS	Rana rugosa (Frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.		
OX	NCBI_TaxId:8410;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	MEDLINE-99083429; PubMed-9866197;		
RA	Miyata I., Ohnishi H., Nakamura M., Ichikawa Y., Saitoh K.:		
RT	"The origin and differentiation of the heteromorphic sex chromosomes		
RT	Z, W, X, and Y in the frog <i>Rana rugosa</i> , inferred from the sequences of		
RT	a sex-linked gene, Adp/ATP translocase."		
RL	Mol. Biol. Evol. 15:1612-1619(1998).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL		
CC	INNER MEMBRANE (BY SIMILARITY).		
CC	-1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.		
DR	EMBL: AB008457; BAA36507.1; -		
DR	InterPro: IPR001993; Mitoch_carrtier.		
DR	InterPro: IPR002067; Mlt_carrtier.		
DR	InterPro: IPR002030; Mlt_uncoupling.		
DR	Pfam: PF00153; mito_catr. 3.		
DR	PRINTS: PR00926; MITOCARRIER.		
DR	PRINTS: PR00784; MTUNCOUPLING.		
DR	PROSITE: PS00215; MITOCH_CARRIER. 3.		
KN	Inner membrane, Mitochondrion; Repeat; Transmembrane; Transport.		
Qc	SEQUENCE 298 AA; 3506 MW; 158270DD37099A00 CRC64;		

[illegible]

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ID 09PRH1      PRELIMINARY;      PRT;      298 AA.
AC 09PRH1;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
NCBI_TaxID=8410;
RX MEDLINE=99083429; PubMed=9866197;
RA Miura T., Ohtani H., Nakamura M., Ichikawa Y., Saichou K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -.
DR EMBL; AB008456; BAA36506.1; -.
DR EMBL; AB008461; BAA36511.1; -.
DR EMBL; AB008462; BAA36512.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

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Query Match      88.7%; Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%; Pred. No. 1.2e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDLFLAGAAVAAVSTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVR 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MTDAAISFADFLAGVAAAIKSTAVAPIERVKLLLOVQHASKOITADKQYKGIIMDCVR 60

QY 61 IPKEOGFLSPWGNLANVITFPQALNFAFKKYYKQLFLGVDRHKQFRRYFAGNLASG 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 IPKEOGFVSFWGNLANVITFPQALNFAFKKYYKQLFLGVDRHKQFRRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTLADVGRR-AQREFHGLGDCIIRIKFSKSGLRGLYOGFNVS 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 GAAGATSLCFVYPLDFARTLADVGKAGADREFKGLGDCIIRIKFSKSGLRGLYOGFNVS 180

QY 180 VGGIIYRAAYFGVYDTAKGMLDPKKNVHIFVSMIAQSTAVAGLSYFPDVTYRRMM 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 VGGIIYRAAYFGIYDTAKGMLDPKKNTHIFISWIAQSTAVAGLSYFPDVTYRRMM 240

QY 240 QSGRKAGDIWYTGVCWKRKIADEGAKAFKFGAMSVNLGKMGAFVLYYDEIKKVV 297
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 QSGRKAGELWYSGTIDCWKRKIADEGSRAPFKGAMSVNLGKMGAFVLYYDEIKKYY 298

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RESULT 5
09PRH2      PRELIMINARY;      PRT;      298 AA.
AC 09PRH2;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
NCBI_TaxID=8410;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura T., Ohtani H., Nakamura M., Ichikawa Y., Saichou K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008460; BAA36510.1; -.
DR EMBL; AB008458; BAA36508.1; -.
DR EMBL; AB008459; BAA36509.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599A06 CRC64;

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Query Match      88.5%; Score 1374.5; DB 13; Length 298;
Best Local Similarity 86.2%; Pred. No. 2.3e-118;
Matches 257; Conservative 24; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDLFLAGAAVAAVSTAVAPIERVKLLLOVQHASKOISAEKQYKGIIDCVR 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MTDAAISFADFLAGVAAAIKSTAVAPIERVKLLLOVQHASKOITADKQYKGIIMDCVR 60

QY 61 IPKEOGFLSPWGNLANVITFPQALNFAFKKYYKQLFLGVDRHKQFRRYFAGNLASG 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 IPKEOGFVSFWGNLANVITFPQALNFAFKKYYKQLFLGVDRHKQFRRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTLADVGRR-AQREFHGLGDCIIRIKFSKSGLRGLYOGFNVS 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 GAAGATSLCFVYPLDFARTLADVGKAGADREFKGLGDCIIRIKFSKSGLRGLYOGFNVS 180

QY 180 VGGIIYRAAYFGVYDTAKGMLDPKKNVHIFVSMIAQSTAVAGLSYFPDVTYRRMM 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 VGGIIYRAAYFGIYDTAKGMLDPKKNTHIFISWIAQSTAVAGLSYFPDVTYRRMM 240

QY 240 QSGRKAGDIWYTGVCWKRKIADEGAKAFKFGAMSVNLGKMGAFVLYYDEIKKVV 297
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 QSGRKAGELWYSGTIDCWKRKIADEGSRAPFKGAMSVNLGKMGAFVLYYDEIKKYY 298

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RESULT 6
0919M9      PRELIMINARY;      PRT;      298 AA.
AC 0919M9;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
DE ADENINE NUCLEOTIDE TRANSLOCASE.
GN ANTI1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RX MEDLINE=99083429; PubMed=9866197;
RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development."
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

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DR EMBL: AF231347; AAF63471.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane: Mitochondrion; Transmembrane; Transport.
 DR SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 88.0%; Score 1366.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 1.2e-117;
 Matches 257; Conservative 23; Mismatches 17; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVVR 60
 DB 1 MTDAAISFKADFLAGVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVVR 60
 OY 61 IPKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 DB 61 IPKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFNV 179
 OY 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFNV 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFNV 180
 OY 180 VGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYFPTVRRRM 239
 DB 180 VGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYFPTVRRRM 239
 OY 240 OSGRKGADIMYGTGVDQWKRKIADEGAKAFKFGAMSNVLRGAGFVLVLYDEIKKYV 297
 DB 240 OSGRKGADIMYGTGVDQWKRKIADEGAKAFKFGAMSNVLRGAGFVLVLYDEIKKYV 297
 OY 241 OSGRKGADIMYGTGVDQWKRKIADEGAKAFKFGAMSNVLRGAGFVLVLYDEIKKYV 298
 DB 241 OSGRKGADIMYGTGVDQWKRKIADEGAKAFKFGAMSNVLRGAGFVLVLYDEIKKYV 298

RESULT 7
 O9NHMS PRELIMINARY: PRT; 300 AA.
 AC O9NHMS;
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE ADP/ATP TRANSLOCASE.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestridae; Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS MAL SEEKING;
 RA Chen Z., Fair J.A., Batterham P.;
 RL "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*,"
 CC Submitted (Dec-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: AF218587; AAF32322.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane: Mitochondrion; Transmembrane; Transport.
 DR SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;
 Best Local Similarity 78.7%; Pred. No. 3.9e-106;
 Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

OY 1 MGDH---WSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDC 57
 DB 1 MGDH---WSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDC 57
 OY 1 MGDH---WSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDC 60
 DB 1 MGDH---WSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDC 60
 OY 58 VRIKKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 117
 DB 58 VRIKKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 117
 OY 61 FVIRKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 120
 DB 61 FVIRKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNL 120
 OY 118 ASGGAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFN 177
 DB 121 ASGGAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFN 180
 OY 178 VSVGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYFPTVRRRM 237
 DB 178 VSVGGIITIRAAVYGVYDTAKGMLPDPKNVHIFVSMIAQSVTAAGLSYFPTVRRRM 237
 OY 238 NMOSGRKGADIMYGTGVDQWKRKIADEGAKAFKFGAMSNVLRGAGFVLVLYDEIKKYV 297
 DB 241 NMOSGRKGADIMYGTGVDQWKRKIADEGAKAFKFGAMSNVLRGAGFVLVLYDEIKKYV 297

RESULT 8
 O91336 PRELIMINARY: PRT; 317 AA.
 ID O91336;
 AC O91336;
 DT 01-NOV-1996 (TREMBLrel. 01, created)
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE ADP/ATP TRANSLOCASE.
 OS Rana sylvatica (wood frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cai Q., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 RL in wood frogs under freezing stress";
 RL Biochim. Biophys. Acta 1353:69-78(1997).
 RN [2]
 RP REVISIONS.
 RA Cai Q., Storey K.B.;
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: U44832; AAA97882.2; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mltc_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane: Mitochondrion; Repeat; Transmembrane; Transport.
 DR SEQUENCE 317 AA; 35005 MW; 5F6B7ED8D5CEB72 CRC64;

Query Match 79.5%; Score 1234.5; DB 13; Length 317;
 Best Local Similarity 85.7%; Pred. No. 1.9e-105;
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDLGAVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVVR 60
 DB 1 MTDAAISFKADFLAGVAAVSKTAVAPIERVKLLQVQHSKQISAEKQYGIIDCVVR 60
 OY 61 IPKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 DB 61 IPKEOGFLSFWGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADYGRRA-QREFHGLGDCIIRKFSGLRGLYGFNV 180

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Bult C.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Botkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gar N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relneert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrstka R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RA Zhang Y.Q., Davis A.W., Roote J., Ashburner M.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003484; AAF47956.1; -;
 DR EMBL: Y10618; CAA71629.1; -;
 DR FlyBase; FBgn0025111; Ant2.
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN 2.
 SQ SEQUENCE 307 AA; 33744 MW; 3D6B3DFD82061C0C CRC64;

Query Match 73.9%; Score 1147; DB 5; Length 307;
 Best Local Similarity 73.8%; Pred. No. 2e-97;
 Matches 214; Conservative 33; Mismatches 43; Indels 0; Gaps 0;

7 SFLKFLGAAVAASKTAAPIERVKLLQVQASKOISAEKYGKGIIDCVVRIPKKEG 66
 17 SFLDMFMGSAALAKTAVAPIERVKLLQVQASKOISADQKRGIVDFIRIPKKEG 76
 67 FLSEFRGNLANVIRYFPQALNFAFKDKYKOLFGLGVDNRHKQFMYFPGNLANSGAAGT 126
 77 FSSFRGNLANVIRYFPQALNFAFKDYKSVFLGVDNRHKQFMYFPGNLANSGAAGT 136
 127 SLCEFYVPLDFARTRLAADVGRRAQREFHGLGDCIIRKFSKDSGLRGLXOGFNVSGIIT 186
 137 SLCEFYVPLDFARTRLAADVGRRAQREFHGLGDCIIRKFSKDSGLRGLXOGFNVSGIIT 196
 187 RAATGCVYDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSGRGA 246
 197 RAATGCVYDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSGRGA 256
 247 DIMYGTGTCMRKIKAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKY 296

Db 257 EMVYKNTAHCVLVIKQEGISAFKGFALSNIRGGALVLYLDEMKKY 306
 RESULT 12
 ID 025129 PRELIMINARY; PRT; 304 AA.
 AC 025129;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADP/ATP TRANSLOCASE.
 GN HRAFL.
 OS Halocynthia roretzi (Sea squirt).
 OC Eukaryota; Metazoa; Chordata; urochordata; Ascidiacea;
 OC Stolidobranchia; Pyrosidae; Halocynthia.
 OX NCBI_TaxID=7729;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Miya T.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Miya T., Makebe K., Satoh N.;
 RT "Expression of a gene for major mitochondrial protein, ADP/ATP
 RT translocase, during embryogenesis in the ascidian *Halocynthia*
 RT roretzi.";
 RL Dev. Growth Differ. 36:39-48(1994).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY)
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: D83069; BA01765.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 304 AA; 33306 MW; 51FD0D7D6B654880 CRC64;

Query Match 73.4%; Score 1139.5; DB 5; Length 304;
 Best Local Similarity 74.6%; Pred. No. 9.6e-97;
 Matches 220; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

6 WS--FLKFLGAAVAASKTAAPIERVKLLQVQASKOISAEKYGKGIIDCVVRIP 62
 3 WSAVDFAKDLAIGTAAAIKTIYAPIERVKLLQVQASVOMKAGTEYKGIIDAFVRIP 62
 63 KEQGFSLMRGNLANVIRYFPQALNFAFKDKYKOLFGLGVDNRHKQFMYFPGNLANSGA 122
 123 AGATSLCEVYPLDFARTRLAADVGRRAQREFHGLGDCIIRKFSKDSGLRGLXOGFNVSG 182
 123 AGATSLCEVYPLDFARTRLAADVGRRAQREFHGLGDCIIRKFSKDSGLRGLXOGFNVSG 182
 183 IIVRAAFGYVDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSG 242
 183 IIVRAAFGYVDTAKGMLPDKRNHIEFVSMIAQSVTAAGLSTPEDTVRRRMMQSG 242
 243 RKGADIMTGTGTCMRKIKAKDEGAKAFKGAWSNVLRGMGAFVLVLYDEIKKY 297
 243 RKKEDRMVTKGYVDCWGIKYNKKGAKFKGALSNVIRGTGALVLYLDEIKKY 297

RESULT 13
 ID 09H0C2 PRELIMINARY; PRT; 315 AA.
 AC 09H0C2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 Search time 22.53 Seconds

(Without alignments)
483.331 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAA.....LRGMGAFVLVLYDEIRKKV 297

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query length	ID	Description
1	1526.5	98.3	298	ADT1_HUMAN	P12235 homo sapien
2	1466.5	94.4	298	ADT1_RAT	Q05962 rattus norv
3	1457.5	93.9	298	ADT1_MOUSE	P48962 mus musculu
4	1453.5	93.6	297	ADT1_BOVIN	P02722 bos taurus
5	1408.5	90.7	298	ADT2_MOUSE	P51881 mus musculu
6	1407.5	90.6	298	ADT2_RAT	Q09073 rattus norv
7	1398.5	90.1	298	ADT2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	ADT3_HUMAN	P12236 homo sapien
9	1380.5	89.9	298	ADT3_BOVIN	P12207 bos taurus
10	1211	78.0	297	ADT1_DROME	Q26365 drosophila
11	1162.5	74.9	301	ADT1_ANOGA	Q27238 anopheles g
12	973.5	62.7	339	ADT1_CHLRE	P31682 chlorella k
13	770.5	49.6	308	ADT1_CHLRE	P27080 chlamydomon
14	756.5	48.7	387	ADT1_MAIZE	P04709 zea mays (m
15	752.5	48.5	322	ADT1_SCHPO	Q09188 schizosacch
16	752.5	48.5	322	ADT1_GOSHI	Q22342 gossypium h
17	751.5	48.4	382	ADT1_ORYSA	P1691 oryza sativ
18	751.5	48.4	387	ADT2_MAIZE	P12857 zea mays (m
19	746	48.0	381	ADT1_ARATH	P31167 arabidopsis
20	744.5	47.9	386	ADT1_SOLTU	P25083 solanum tub
21	742.5	47.8	331	ADT1_WHEAT	Q41629 triticum ae
22	740	47.6	386	ADT2_SOLTU	P27081 solanum tub
23	737	47.5	385	ADT2_ARATH	P40941 arabidopsis
24	736	47.4	307	ADT3_YEAST	P18238 saccharomyc
25	734	47.3	318	ADT2_YEAST	P18239 saccharomyc
26	733.5	47.2	313	ADT1_NEUCR	P02723 neurospora
27	729	46.9	305	ADT1_KLULA	P49382 kluyveromyc
28	728.5	46.9	331	ADT2_WHEAT	Q41630 triticum ae
29	718.5	46.3	309	ADT1_YEAST	P45760 saccharomyc
30	302.5	19.5	678	CMC1_HUMAN	Q75746 homo sapien
31	300.5	19.3	330	GDC_BOVIN	Q01888 bos taurus
32	296.5	19.1	702	CMC1_CAEL	Q21133 caenorhabdl
33	296	19.1	588	CMC2_CAEL	Q20799 caenorhabdl

34	295	19.0	322	1	GDC_RAT	P16261 rattus norv
35	292.5	18.8	307	1	YOTL_YEAST	Q99297 saccharomyc
36	292	18.8	332	1	GDC_HUMAN	P16260 homo sapien
37	291	18.7	675	1	CMC2_HUMAN	Q94500 homo sapien
38	286	18.4	587	1	CMC3_CAEL	Q19329 caenorhabdl
39	279.5	18.0	676	1	CMC2_MOUSE	Q94504 mus musculu
40	267.5	17.2	322	1	BMCP_MOUSE	Q92282 mus musculu
41	265.5	17.1	325	1	BMCP_HUMAN	Q92288 homo sapien
42	263.5	17.0	695	1	CMC1_DROME	Q94732 drosophila
43	258.5	16.6	326	1	YEOB_SCHPO	Q13805 schizosacch
44	248.5	16.0	324	1	PMT_YEAST	P32332 saccharomyc
45	246	15.8	436	1	BTL_MAIZE	P29518 zea mays (m

ALIGNMENTS

RESULT 1	ADT1_HUMAN	STANDARD:	PRT:	298 AA.
AC	P12235:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	ADP, ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP			
DE	TRANSLUCASE 1) (ADENINE NUCLEOTIDE TRANSLUCATOR 1) (ANT 1).			
GN	SIC25M4 OR ANT1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89236396; PubMed=2541251;			
RA	Cozens A.L., Runswick M.J., Walker J.E.;			
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial			
RT	ADP/ATP translocase.";			
RL	J. Mol. Biol. 206:261-280(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89340499; PubMed=2823266;			
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,			
RA	Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;			
RT	"A human muscle adenine nucleotide translocator gene has four exons,			
RT	RT is located on chromosome 4, and is differentially expressed.";			
RL	J. Biol. Chem. 264:13998-14004(1989).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88041149; PubMed=2823266;			
RA	Neckermann N., Li K., Wade R.P., Shuster R., Wallace D.C.;			
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack			
RT	of a leader peptide, divergence from a fibroblast translocator cDNA,			
RT	and coevolution with mitochondrial DNA genes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).			
RN	[4]			
RP	SEQUENCE OF 1-37 FROM N.A.			
RC	TISSUE=Liver;			
RX	MEDLINE=88124845; PubMed=2829183;			
RA	Houldsworth J., Attardi G.;			
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA			
RT	level in adult human liver.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).			
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE			
CC	MITOCHONDRIAL INNER MEMBRANE.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL			
CC	INNER MEMBRANE.			
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC or send an email to license@isb-sib.ch).

DR EMBL: J02966; AAA61223.1; -
DR EMBL: J03593; AAA36751.1; -
DR EMBL: J04982; AAA51736.1; -
DR PIR: A28116; A28116.
DR PIR: A39891; A39891.
DR PIR: S03893; S03893.
DR PIR: A44778; A44778.
DR MIM: I03220; -
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; Mitoch_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
ET REPEAT 1 110 1.
ET REPEAT 111 208 2.
ET REPEAT 209 298 3.
ET REPEAT 209 298 3.
ET CONFLICT 16 16 G-> A (IN REF. 3).
ET CONFLICT 147 149 KGA-> RR (IN REF. 3).
ET CONFLICT 227 227 V-> L (IN REF. 3).
SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAECA7CFFBB CRC64;

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 1.8e-131;
Matches 293; Conservative 2; Mismatches 13; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGVAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
DB 1 MGDHANSFLKDFLAGVAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
QY 61 IPKEOGFLSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQWRFFAGNLASG 120
DB 61 IPKEOGFLSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQWRFFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 179
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 180
QY 180 VGGIIRYRAAYGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSTPFTVRRRMM 239
DB 180 VGGIIRYRAAYGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSTPFTVRRRMM 240
QY 240 OSGRKADIMYGTVDWCRRKIAKDEGAKAFPGAMSNVLRGNGAFVLVLYDEIKKYV 297
DB 240 OSGRKADIMYGTVDWCRRKIAKDEGAKAFPGAMSNVLRGNGAFVLVLYDEIKKYV 298

RESULT 2
ADT1_RAT STANDARD; PRT; 298 AA.
ID ADT1_RAT
AC 005962;
DT 01-FEB-1994 (Rel. 28. Created)
DT 01-FEB-1994 (Rel. 28. Last sequence update)
DT 20-AUG-2001 (Rel. 40. Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLCASE 1) (ADENINE NUCLEOTIDE TRANSLCATOR 1) (AMT 1).
GN SIC25A4 OR ANTL.
OG Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY, AND WISTAR; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC - FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC - SUBUNIT: HOMODIMER.
CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC - TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.
CC - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL: X61667; CAA43842.1; -
DR EMBL: D12770; BAA02237.1; -
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
ET REPEAT 1 110 1.
ET REPEAT 111 208 2.
ET REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 94.4%; Score 1466.5; DB 1; Length 298;
Best Local Similarity 94.3%; Pred. No. 5.1e-126;
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHANSFLKDFLAGVAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
DB 1 MGDHANSFLKDFLAGVAANAASKTAVAPIERVKLLQVOHASKOISAEKQYGIIDCVVR 60
QY 61 IPKEOGFLSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQWRFFAGNLASG 120
DB 61 IPKEOGFLSFWMGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQWRFFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 179
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAOREFHGLGDCIIRKFSDDLRLGLYGFNV 180
QY 180 VGGIIRYRAAYGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSTPFTVRRRMM 239
DB 180 VGGIIRYRAAYGVYDTAGKMLPDPKNVHIIFVSMIAOSVTAAGLVSTPFTVRRRMM 240
QY 240 OSGRKADIMYGTVDWCRRKIAKDEGAKAFPGAMSNVLRGNGAFVLVLYDEIKKYV 297
DB 240 OSGRKADIMYGTVDWCRRKIAKDEGAKAFPGAMSNVLRGNGAFVLVLYDEIKKYV 298

ADTL_MOUSE	3	RESULT
ID	ADTL_MOUSE	STANDARD: PRT: 298 AA.
AC	P48962;	
DT	01-FEB-1996 (Rel. 33, Created)	
DT	01-FEB-1996 (Rel. 33, Last sequence update)	
DT	20-AUG-2001 (Rel. 40, Last annotation update)	
DE	ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP	
DE	TRANSLACASE 1) (ADENINE NUCLEOTIDE TRANSLACATOR 1) (ANT 1;.	
CN	SIC25A4 OR ANTL.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
OX	NCBI_Taxid=10090;	
RP	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=C57BL/6; TISSUE=Brain;	
RX	MEDLINE=97059403; PubMed=8903724;	
RA	Ellison J.W., Li X., Francke U., Shapiro L.J.;	
RT	"Rapid evolution of human pseudautosomal genes and their mouse	
RT	homologs."	
RL	Mamm. Genome 7:25-30(1996).	
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE	
CC	MITOCHONDRIAL INNER MEMBRANE.	
CC	-1- SUBUNIT: HOMODIMER.	
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL	
CC	INNER MEMBRANE.	
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.	
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.	
CC	-----	
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CC	use by non-profit institutions as long as its content is in no way	
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/).	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; U27315; AAC52837.1; -.	
-DR	MGI; MGI:1353495; SIC25a4.	
DR	InterPro: IPR002067; Mito_carrier.	
DR	InterPro: IPR001993; Mitoch_carrier.	
DR	Pfam; PF00153; mito_carr; 3.	
DR	PRINTS; PR00926; MITOCARRIER.	
DR	PRINTS; PR00927; ADPTRNSLASE.	
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.	
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;	
KW	Multisene family.	
KW	TRANSMEM 12 29 1 (POTENTIAL).	
FT	TRANSMEM 73 91 2 (POTENTIAL).	
FT	TRANSMEM 117 134 3 (POTENTIAL).	
FT	TRANSMEM 176 195 4 (POTENTIAL).	
FT	TRANSMEM 214 231 5 (POTENTIAL).	
FT	TRANSMEM 273 291 6 (POTENTIAL).	
FT	REPEAT 1 110 1.	
FT	REPEAT 111 208 2.	
FT	REPEAT 209 298 3.	
FT	SEQUENCE 298 AA; 32870 MW; 32ACB34EFC4F482 CRC64;	
SO		
Query Match	93.9%; Score 1457.5; DB 1; Length 298;	
Best Local Similarity	93.6%; Pred. No. 3,4e-125;	
Matches 279;	Conservative 10; Mismatches 8; Indels 1; Gaps 1;	
QY	1 MGDHAWSLKDFLAGAVALAAVSKTAVAPIERVKLLLYOVHASKOISAEKQYGIIDCVVR 60	
DB	1 MGDQALSLKDFLAGAGIAAAVSKTAVAPIERVKLLLYOVHASKOISAEKQYGIIDCVVR 60	
OY	61 IPKGGGSLFWNGNLANYRVRFQTALNFAFDKTKQLFLGVDVDRHKQWRWFAGNLASG 120	
DB	61 IPKGGGSLFWNGNLANYRVRFQTALNFAFDKTKQLFLGVDVDRHKQWRWFAGNLASG 120	

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OY 121 GAAGTSTLCFVYPLDFAFTRLAADYGR -RAOREPHGLGDCIIKIFKSGGLGKVGFNVS 179
Db 121 GAGATSTSLCFVYPLDFAFTRLAADYAGKSSQREFNGLEDCLKIFKISGGLGKVGGSVS 180
OY 180 VGGIITVYAAAFVGVYDTAKKGLPDPKNNVHIFVSNMIAQSVTAVALGLSTYPPDFTVRRMM 239
Db 181 VGGIITVYAAAFVGVYDTAKKGLPDPKNNVHIIYSNMIAQSVTAVALGLSTYPPDFTVRRMM 240
OY 240 QSGRKAGADIMTGTIVDCNRKIAKDEGAKAFKFGKANSNLRGNGCAFVLVYDEIKKY 297
Db 241 QSGRKAGADIMTGTIVDCNRKIAKDEGANAAFFKGSANSNLRGNGCAFVLVYDEIKKY 298

RESULT 4
ADT1_BOVIN STANDARD: PRT: 297 AA.
ID ADT1_BOVIN
AC P02722:
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE 1)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (bovine).
OC Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE.
RX MEDLINE=82188267; PubMed=7076130;
RA Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE=86295775; PubMed=3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -I- SUBUNIT: HOMODIMER.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M13783; AAA30363.1; -.
DR EMBL: M24102; AAA30768.1; -.
DR PIR: A03181; XMBO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; MltOch_carrier.

```

DR Pfam: PF00153; mito_carr: 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSICASE.
 DR PROSITE: PS00215; MITOCH_CARRIER: 3.
 DR Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Methylation.
 FT INIT_MER 0 0
 FT MOD_RES 1 1 BLOCKED.
 FT MOD_RES 51 51 METHYLATION (POTENTIAL).
 FT TRANSMEM 11 28 1 (POTENTIAL).
 FT TRANSMEM 72 90 2 (POTENTIAL).
 FT TRANSMEM 116 133 3 (POTENTIAL).
 FT TRANSMEM 175 194 4 (POTENTIAL).
 FT TRANSMEM 213 230 5 (POTENTIAL).
 FT TRANSMEM 272 290 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 207 2.
 FT REPEAT 208 297 3.
 FT SEQUENCE 297 AA: 32836 MW: A582D3C4A40AEB48 CRC64;

Query Match 93.6%; Score 1453.5; DB 1; Length 297;
 Best Local Similarity 94.6%; Pred. No. 7.8e-125;
 Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 3 DHAMSLKDFLAGAANAASKTAVADIERVKLLQYOHASKOISAEKQYKGIIDCVVRIP 62
 DB 2 DQALSLKDFLAGGVAASIKSTAVADIERVKLLQYOHASKOISAEKQYKGIIDCVVRIP 61
 OY 63 KEEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASGA 122
 DB 62 KEEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASGA 121
 OY 123 AGATSLCFVYPLDFARTRLAADVGR-AQREFHGLDCIIRKSGRLGYGFNVSVQ 181
 DB 122 AGATSLCFVYPLDFARTRLAADVGR-AQREFHGLDCIIRKSGRLGYGFNVSVQ 181
 OY 182 GIITTYAATFGVYDTAKGMLPDKNVHIFVSMIAQTVAAVLVSPEDTVRRMMOS 241
 DB 182 GIITTYAATFGVYDTAKGMLPDKNVHIFVSMIAQTVAAVLVSPEDTVRRMMOS 241
 OY 242 GRRGADIMYTGTVDCMKRIAKDEGAKAFKGSANVLRGSGAFVLYLDEIKKYV 297
 DB 242 GRRGADIMYTGTVDCMKRIAKDEGAKAFKGSANVLRGSGAFVLYLDEIKKYV 297

RESULT 5
 ADP2_MOUSE STANDARD: PRT: 298 AA.
 ID ADP2_MOUSE
 AC P51881; 061311; Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADP, ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
 DE (ADONINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
 GN SL25A5 OR ANT2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs".
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=skeletal muscle;
 RA Sheldon J.G.;
 RL Theists (1995), University of Cambridge, U.K.

RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RA Costet P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC
 CC EMBL: U27316; AAC52838.1; -
 CC EMBL: U10404; AAL19009.1; -
 CC EMBL: X70847; CAA50196.1; -
 CC MGD: MGI:1353496; Slc25a5.
 DR InterPro: IPR002067; Mit_carr.
 DR InterPro: IPR001993; Mitoch_carr.
 DR Pfam: PF00153; mito_carr: 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSICASE.
 DR PROSITE: PS00215; MITOCH_CARRIER: 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT SEQUENCE 298 AA: 32931 MW: 0798E04B987EFE20 CRC64;

Query Match 90.7%; Score 1408.5; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 9.5e-121;
 Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;

OY 1 MGHAMSLKDFLAGAANAASKTAVADIERVKLLQYOHASKOISAEKQYKGIIDCVVR 60
 DB 1 MTDAAVSFANDFLAGVAASIKSTAVADIERVKLLQYOHASKOISAEKQYKGIIDCVVR 60
 OY 61 IPKEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
 DB 61 IPKEGFLSEFRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKQFWRFFAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLDCIIRKSGRLGYGFNVSVQ 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AQREFHGLDCIIRKSGRLGYGFNVSVQ 180
 OY 180 VCGIITTYAATFGVYDTAKGMLPDKNVHIFVSMIAQTVAAVLVSPEDTVRRMM 239
 DB 181 VCGIITTYAATFGVYDTAKGMLPDKNVHIFVSMIAQTVAAVLVSPEDTVRRMM 240
 OY 240 QSGRKGADIMYTGTVDCMKRIAKDEGAKAFKGSANVLRGSGAFVLYLDEIKKYV 296
 DB 241 QSGRKGADIMYTGTVDCMKRIAKDEGAKAFKGSANVLRGSGAFVLYLDEIKKYV 297


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RESULT 6
ADT2_RAT 6
ID ADT2_RAT STANDARD: PRT: 298 AA.
AC 009073:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SURELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
CC SKELETAL MUSCLE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb.slb.ch).
CC -----
CC CC
CC BR EMBL: D12771; BAA02238.1;
CC DR InterPro: IPR002067; Mlt_carrier.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mito_carr.3
CC DR PRINTS: PR00926; MITOCARRIER.
CC DR PROSITE: PS00215; MITOCH_CARRIER; 3.
CC KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC Multigene family.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 73 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 111 1.
CC FT REPEAT 112 208 2.
CC FT REPEAT 209 298 3.
CC FT SEQUENCE 298 AA; 32901 MW; 6A59204B987EFC3 CRC64;
SO QUERY MATCH
Best Local Similarity 90.6%; Score 1407.5; DB 1; Length 298;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;
QY 1 MGDHANSFLKDLGAVAAVAAVSKTAAVPIERVLLLLQVHASKQISAEKQGIIDCVR 60
DB 1 MTDAAVSFADFLAGGVAAMISKTAAPIERVKLLQVHASKQITADKQYKGIIDCVR 60
QY 61 IPEQGFSLWBRGNLANVIRYPTQALNFAFKKQYKQFLGVDGRHKQFRRYRAGNLASG 120
DB 61 IPEQGVSLWBRGNLANVIRYPTQALNFAFKKQYKQIFLGVDKRTQFWRYPAGNLASG 120

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QY 121 GAAGATSLCFVYPLDFAFRTPLADYGR-AGREFHGLGDCIIKIFKSDGLRGLYOGPNVS 179
DB 121 GAAGATSLCFVYPLDFAFRTPLADYGR-AGREFHGLGDCIIKIFKSDGLRGLYOGPNVS 180
QY 180 VQGIITRYRAAFGVYDTAKMLDPPKRVHIFVSMIAQSVTAAGLLSYFDFVRRMM 239
DB 181 VQGIITRYRAAFGVYDTAKMLDPPKRVHIFVSMIAQSVTAAGLLSYFDFVRRMM 240
QY 240 QSRKGGADWYGTGVDCKRIADDEGAKAFKGAWSNVLRGMGAFVLYDEIKKY 296
DB 241 QSRKGGADWYGTGVDCKRIADDEGAKAFKGAWSNVLRGMGAFVLYDEIKKY 297
RESULT 7
ADT2_HUMAN
ID ADT2_HUMAN STANDARD: PRT: 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baesera R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence.";
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.-T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated.";
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.-N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
RA Mazarrella R.A., Schlessinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozerisky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houlsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SURELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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DR EMBL: M57424; AAA51737.1; -
 DR EMBL: J02683; AAA35579.1; -
 DR EMBL: L78810; AAB39266.1; -
 DR EMBL: AC004000; AAB96347.1; -
 DR EMBL: J03591; AAA36749.1; -
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR MIM: 300150; -
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSICASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.

FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 129 298 3.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 90.1%; Score 1398.5; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 7.7e-120;
 Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDLAVAAVAAVSKTAVAPIERYKLLQVQHASQISAERKQYGIIDCYVR 60
 DB 1 MTDAAVSFAKDLAVAAVAAVSKTAVAPIERYKLLQVQHASQISAERKQYGIIDCYVR 60
 QY 61 IPKEGGLSFWMGNLANVIRYPTQALNFAFKDKYKQFLGSGVDRHKOFRYFAGNLSG 120
 DB 61 IPKEGGLSFWMGNLANVIRYPTQALNFAFKDKYKQFLGSGVDRHKOFRYFAGNLSG 120
 QY 121 GAAGATSLCFVYPLDPARRLADYGR-AOREPHGLGDCIIKIRKSDGLRGYGFNVS 179
 DB 121 GAAGATSLCFVYPLDPARRLADYGR-AOREPHGLGDCIIKIRKSDGLRGYGFNVS 179
 QY 180 VGGIIYRAAYFGVYDTAKGMLDPRKNVHIFVSMIAQSVTAAGILSYPTFVRMM 239
 DB 180 VGGIIYRAAYFGVYDTAKGMLDPRKNVHIFVSMIAQSVTAAGILSYPTFVRMM 239
 QY 240 OSGRKADIMTGYTDCMRKIKADGAKAFKFGANSNVLKRGAGAVLVYDEIKKY 296
 DB 240 OSGRKADIMTGYTDCMRKIKADGAKAFKFGANSNVLKRGAGAVLVYDEIKKY 296
 QY 241 OSGRKGTIDIMYGTLDGCMRKIARDEGKAFKFGANSNVLKRGAGAVLVYDEIKKY 297
 DB 241 OSGRKGTIDIMYGTLDGCMRKIARDEGKAFKFGANSNVLKRGAGAVLVYDEIKKY 297

RESULT 8
 ADT3_HUMAN STANDARD: PRT; 298 AA.
 AC P12236;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADP-ATP CARRIER PROTEIN, LIVER ISOFORM 12 (ADP/ATP TRANSLOCASE 3)
 DE (ADENINE NUCLEOTIDE TRANSLCATOR 3) (ANT 3).
 GN SLC35A6 OR ANT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89236396; PubMed=2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC or send an email to license@isb-sib.ch).

DR EMBL: J03592; AAA36750.1; -
 DR PIR: S03894; S03894.
 DR PIR: B28116; B28116.
 DR MIM: 300151; -
 DR MIM: 403000; -
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSICASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.

FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 2).
 SQ SEQUENCE 298 AA; 32866 MW; 1B534E9F0E49672F CRC64;

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.2e-118;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDLAVAAVAAVSKTAVAPIERYKLLQVQHASQISAERKQYGIIDCYVR 60
 DB 1 MWDQAISFAKDLAVAAVAAVSKTAVAPIERYKLLQVQHASQISAERKQYGIIDCYVR 60
 QY 61 IPKEGGLSFWMGNLANVIRYPTQALNFAFKDKYKQFLGSGVDRHKOFRYFAGNLSG 120
 DB 61 IPKEGGLSFWMGNLANVIRYPTQALNFAFKDKYKQFLGSGVDRHKOFRYFAGNLSG 120
 QY 121 GAAGATSLCFVYPLDPARRLADYGR-AOREPHGLGDCIIKIRKSDGLRGYGFNVS 179
 DB 121 GAAGATSLCFVYPLDPARRLADYGR-AOREPHGLGDCIIKIRKSDGLRGYGFNVS 179

Matches	259:	Conservative	21:	Mismatches	17:	Indels	1:	Gaps	1:
QY	1	MGDIHWSFLKDFPLGVAANAASKTAVAPIERYKLLLOVOHASKQISAEKQKGIIDCYVR	60						
Db	1	MTEQAIISPAKFFDFLAGGIAAIAISKTAVAPIERYKLLLOVOHASKQIAAOKYQYGIIDCYVR	60						
QY	61	IPKEGGLSEPMRGNLANIYRFPPTQALNPAFADKXKQYFLIGVDHDKQPMWRFAGNLASG	120						
Db	61	IPKEGGLSEPMRGNLANIYRFPPTQALNPAFADKXKQYFLIGVDHDKQPMWRFAGNLASG	120						
QY	121	GAAGATSLCFYVPLDFAFTRLAADYGR - ADRFPHGLDCIIRKPSDGLRGLYOGFNVS	179						
Db	121	GAAGATSLCFYVPLDFAFTRLAADYGRSGSREFRGLDCIIRKPSDGLRGLYOGFNVS	180						
QY	180	VOGIIITTAATFQYVDTAKGMLPDPKKNHIFVSMHIAOSYTAAGLSLSPFTVRRRMM	239						
Db	181	VOGIIITTAATFQYVDTAKGMLPDPKKNHIVSMIAOTVTAAGVSVSPFTVRRRMM	240						
QY	240	QSGRGADIMYTGATYDCNRKIADGAKAFKFGAMSNVLRGGAFAVLVYDEIRKYV	297						
Db	241	QSGRGADIMYTGATYDCNRKIADGAKAFKFGAMSNVLRGGAFAVLVYDELKKVI	298						
RESULT	10								
ADT_DROME		STANDARD:	PRT:	297	AA.				
ID	ADT_DROME								
AC	Q26365:	Q26254:	P91614:	Q9VZ70:					
DT	15-JUL-1998	(Rel. 36, Created)							
DT	15-JUL-1998	(Rel. 36, Last sequence update)							
DT	20-AUG-2001	(Rel. 40, Last annotation update)							
DE	ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE								
DE	TRANSLOCATOR) (ANT) (STRESS SENSITIVE B PROTEIN).								
GN	SESB OR A/A-T OR CG16944.								
OS	Drosophila melanogaster (Fruit fly).								
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;								
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;								
OC	Ephydroidea; Drosophilidae; Drosophila.								
OX	NCBI_TaxID:7227;								
LN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=92389367; PubMed=1387687;								
RA	Louvi A., Tsitilou S.G.;								
RT	"A cDNA clone encoding the ADP/ATP translocase of Drosophila								
RT	melanogaster shows a high degree of similarity with the mammalian								
RT	ADP/ATP translocases.";								
RL	J. Mol. Evol. 35:44-50(1992).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=94350065; PubMed=7520869;								
RA	Hutler P., Karch F.;								
RT	"Molecular analysis of a candidate gene for the reproductive								
RT	isolation between sibling species of Drosophila.";								
RL	Experientia 50:749-762(1994).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=ORECON-R;								
RL	Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;								
RL	submitted (Jan-1997) to the EMBL/Genbank/DBJ databases.								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=BERKELEY;								
RX	MEDLINE=20196006; PubMed=10731132;								
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,								
RA	Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,								
RA	George R.A., Lewis S.E., Richards S.D., Ashburner M., Henderson S.N.,								
RA	Sturgeon G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,								
RA	Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,								
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,								
RA	Abbill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,								
RA	Ballem R.M., Basos A., Bendandi J., Bayraktaroglu L., Beasley E.M.,								
RA	Beeson K.Y., Beeson P.V., Bernan B.P., Bhandari D., Bolshakov S.,								
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,								


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QY 183 IIVRAVFGVYDTAK-----GMLPDKNVHIFVSMIAQSVTAAGLLSPEDTVRRM 237
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 265 IIVRGIFGLYSIKRIVLTGNLD-----NFFASFLGMLITNGAGLAPIDTVRRM 320

QY 238 MMSGKRGADIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGMAFVLVYDEIK---- 293
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 321 MMTSGEA---VKYKSSIDARQQLIKKEGPKSLFKGAGANILRAIAGAGVLSGVDOQLTF 377

QY 294 --KKY 296
   ||:|
Db 378 FGKKY 382

RESULT 15
ADT_SCHPO STANDARD: PRT: 322 AA.
ID ADT_SCHPO STANDARD: PRT: 322 AA.
AC 009188;
AT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE ADP ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
   TRANSLOCATOR) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=96257204; PubMed=8675018;
RA Cousin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
   carrier of Schizosaccharomyces pombe by functional complementation in
   Saccharomyces cerevisiae."
RL Gene 171:113-117(1996).
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
   Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
   MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY)
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
   INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL: Z49974; CAA90275.1; .
DR EMBL: AL023634; CAA19176.1; -.
DR HSSP: P04002; IATF.
DR InterPro: IPR002067; Mit_Carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 28 48 111 1
FT TRANSMEM 93 111 2 (POTENTIAL).
FT TRANSMEM 131 151 3 (POTENTIAL).
FT TRANSMEM 197 217 4 (POTENTIAL).
FT TRANSMEM 242 242 5 (POTENTIAL).

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FT TRANSMEM 289 309 6 (POTENTIAL).
SQ SEQUENCE 322 AA; 35020 MM; 8AC3D16A40F41AFC CRC64;

Query Match 48.5%; Score 752.5; DB 1; Length 322;
Best Local Similarity 52.9%; Pred. No. 4e-61;
Matches 156; Conservative 51; Mismatches 75; Indels 13; Gaps 6;

QY 7 SFLKDFLAGAVAAVSTAVAPIERVKLLQVOHASKOISAER---QYKGIIDCVARIIPK 63
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 26 TFFDFPMGGSAAVSKTAAAPIERVKLLIQNQ--DEMIRAGRLSHRYKGIIECFKRTAA 83

QY 64 EOGFLSPMRCNLAVIRYPTQALNFAFKDKYKQFLGVDVRHKQFMRYPAGNLAGGAA 123
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 84 EGVYISLRGNNTAVLVYFTQALNFAFKDKYKMF-GYKKERDGIKMRAGNLAGGAA 142

QY 124 GATSLCFVYPLDFARTRLAAD---VGRRAQREFHGLDCIIRKSDGLRGYOGFNVSV 180
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 143 GAASLLEFVYSLDYARTRLANDAKSARKGERQFGLVDYVRKTYRSDGLRGYRFGPSV 202

QY 181 QGIIYRAAFEGYVDTAKG-MLEDPKNVHIFVSMIAQSVTAAGLLSPEDTVRRMM 239
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 203 VGIVYRGLYFGMDTLKPVLVGPLEGNFLASFLGMAVTTGSGVASYPDLTIRRRMM 262

QY 240 QSGRKGADIMYTGTVDCMRKIAKDEGAKAFKGAWSNVLRGMAFVLVYDEIK 294
   ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:| ||:|
Db 263 TSGEA---VKYSSFEGRQILAKEGARSEFKGAGANIILGAGVLSITDOVO 314

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Search completed: February 13, 2002, 09:34:42
Job time: 199 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 ; Search time 34.78 Seconds
(without alignments)
650.484 Million cell updates/sec

Title: US-09-393-441-31

Sequence: 1 MGDHWSFLKDFLAGAVAAA.....LRGMGAFVLYDEIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1526.5	98.3	298	1 A44778	ADP/ATP carrier pr
2	1466.5	94.4	298	2 160173	adenine nucleotide
3	1463.5	94.2	298	2 S37210	ADP/ATP carrier pr
4	1458.5	93.9	298	1 XWBO	ADP/ATP carrier pr
5	1391.5	89.2	298	1 A29132	ADP/ATP carrier pr
6	1385.5	89.2	298	1 S03894	ADP/ATP carrier pr
7	1380.5	88.9	298	2 B43646	ADP/ATP carrier pr
8	1368.5	88.1	298	2 S31814	ADP/ATP carrier pr
9	1142.5	73.6	301	1 S31935	ADP/ATP carrier pr
10	1045.5	67.3	313	2 T25850	hypothetical prote
11	1043.5	67.2	313	2 T23207	hypothetical prote
12	1037.5	66.8	300	2 T25371	hypothetical prote
13	1005.5	64.7	300	2 T15206	hypothetical prote
14	973.5	62.7	339	2 A41677	ADP/ATP carrier pr
15	904.5	58.2	301	2 S51132	ADP/ATP carrier pr
16	772	49.7	306	2 T20012	hypothetical prote
17	770.5	49.6	308	1 S30259	ADP/ATP carrier pr
18	756.5	48.7	387	2 S14876	ADP/ATP carrier pr
19	752.5	48.5	322	2 T40526	adp/atp translocas
20	752.5	48.5	386	2 T09709	ADP/ATP carrier pr
21	751.5	48.4	387	2 S16568	ADP/ATP carrier pr
22	746.5	48.1	379	2 T04608	ADP/ATP carrier pr
23	746.5	48.1	382	2 S33630	ADP/ATP carrier pr
24	745.5	48.0	326	2 T25728	hypothetical prote
25	745.5	48.0	386	2 S17917	ADP/ATP carrier pr
26	744.5	47.9	386	2 S21974	ADP/ATP carrier pr
27	740	47.6	379	2 S21313	ADP/ATP carrier pr
28	740	47.6	386	2 S14874	ADP/ATP carrier pr
29	737	47.5	385	1 S29852	ADP/ATP carrier pr

30	736	47.4	307	2 A36582	ADP/ATP carrier pr
31	734	47.3	318	1 A31978	ADP/ATP carrier pr
32	733.5	47.2	313	1 XWNC	ADP/ATP carrier pr
33	729	46.9	305	2 S68154	ADP/ATP carrier pr
34	728.5	46.9	306	2 T42011	ADP/ATP carrier pr
35	718.5	46.3	309	2 A24849	ADP/ATP carrier pr
36	676	43.5	298	2 T24029	hypothetical prote
37	508	32.7	327	2 T51577	ADP/ATP translocas
38	368	23.7	415	2 T48171	hypothetical prote
39	367.5	23.7	325	2 T04273	hypothetical prote
40	363	23.4	381	2 T51158	hypothetical prote
41	350.5	22.6	475	2 T50686	peroxisomal Ca-dep
42	349.5	22.5	352	2 T01729	mitochondrial solu
43	345.5	22.2	358	2 T45934	hypothetical prote
44	334.5	21.5	348	2 D84798	probable mitochond
45	327	21.1	332	2 T47703	Ca-dependent solut

ALIGNMENTS

RESULT 1
A44778
ADP/ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP/ATP translocase 1
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence, revision 17-Mar-2000 #text, change 17-Mar-2000
C:Accession: A44778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, J. Biol. Chem. 264, 13998-14004, 1989
A>Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: A44778; M0ID:89340499
A:Accession: A44778
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; M0ID:q178658; P0ID:AAA51736.1; P0ID:q178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; M0ID:8926396
A:Accession: S03893
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A>Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; M0ID:88041149
A:Accession: A39891
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:J02956; M0ID:q339919; P0ID:AAA61223.1; P0ID:q339920
R:Howdsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; M0ID:88124845
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOV>
A:Cross-references: GB:J03593; M0ID:q339724; P0ID:AAA6751.1; P0ID:q339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-296/Protein: ADP/ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>

A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RNAS>
 A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R:Aquila, H.; Mistr, D.; Bullitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A03181; MUID:82188267
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 2-51, 'x', '53-70', 'x', '72-109', 'x', '111-298' <ACU>
 A:Note: residue 52 may be methyllysine
 R:Babel, W.; Machter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A61343; MUID:82046808
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Messon, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3H)-azido-4-Isopropylacridone labels Cys159 of the bovine mitochondrial ADP/ATP carrier
 A:Reference number: S69369; MUID:95172058
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63;154-168 <OET>
 A:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

* Query Match 93.9%; Score 1458.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 1.4e-124;
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDAASFLKDFLAGAANAASVSTAVAPTRERVLLOVQASHASQISAEKQKGLIDCVR 60
 DB 1 MSQALSPFLKDFLAGAANAISKTAAPIERVKLLQVQASHASQISAEKQKGLIDCVR 60
 QY 61 IPKEQGLFSFWRGNLANVIRYPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASG 120
 DB 61 IPKEQGLFSFWRGNLANVIRYPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 180
 QY 180 VQGIITIRAYRFEVYDTAKMLPDPKKNVHTFVSMIAQSTAAVAGLTSYFDFVRRMM 239
 DB 181 VQGIITIRAYRFEVYDTAKMLPDPKKNVHTFVSMIAQSTAAVAGLTSYFDFVRRMM 240
 QY 240 QSGRKAGDIWYTGTCVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 297
 DB 241 QSGRKAGDIWYTGTCVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 298

RESULT 5
 A29132
 ADP/ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C8116
 R:Batini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.

J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regu
 A:Reference number: A29132; MUID:87166056
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:9179246; PIDN:AAA5579.1; PID:9179247
 R:Houdsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', '67-110', 'L', '112-161', 'G', '163-298' <HOU>
 A:Cross-references: GB:J03591; NID:9339720; PIDN:AAA36749.1; PID:9339721
 A:Experimental source: Clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-Xq26
 A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

* Query Match 89.6%; Score 1391.5; DB 1; Length 298;
 Best Local Similarity 88.6%; Pred. No. 1.6e-118;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDAASFLKDFLAGAANAASVSTAVAPTRERVLLOVQASHASQISAEKQKGLIDCVR 60
 DB 1 MTPAASFLKDFLAGAANAISKTAAPIERVKLLQVQASHASQISAEKQKGLIDCVR 60
 QY 61 IPKEQGLFSFWRGNLANVIRYPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASG 120
 DB 61 IPKEQGLFSFWRGNLANVIRYPTQALNFAFKDKYKOLFSGVDRHKOFRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-RAQREFHGLDCTIIFKSDGLRGLYQGFNV 180
 QY 180 VQGIITIRAYRFEVYDTAKMLPDPKKNVHTFVSMIAQSTAAVAGLTSYFDFVRRMM 239
 DB 181 VQGIITIRAYRFEVYDTAKMLPDPKKNVHTFVSMIAQSTAAVAGLTSYFDFVRRMM 240
 QY 240 QSGRKAGDIWYTGTCVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 296
 DB 241 QSGRKAGDIWYTGTCVDCWRKRIADDEGAKAFKGAWSNVLRGMGAFVLYYDEIKKY 297

RESULT 6
 S03894
 ADP/ATP carrier protein T3 - human
 N:Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP,
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: S03894; B28116
 R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
 J. Mol. Biol. 206, 261-280, 1989
 A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
 A:Reference number: S03893; MUID:89226336
 A:Accession: S03894
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-298 <COZ>
 R:Houdsworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845
 A:Accession: B28116

Query Match	88.9%	Score 1380.5	DB 2	Length 298
Best Local Similarity	86.9%	Pred No. 1,6e-117		
Matches	259	Conservative	21	Mismatches 17
			Indels	1
			Gaps	1
OY	1	MGDHMSFLKDPDLAAGVAAVAASKTAVAPLPERKLLLOVOHASKQISAEQYKGIIDCVYR	60	
	1		60	
	1		60	
DB	1	MEQATISRFKDPDLAAGIATAISKTAAPLPERKLLLOVOHASKQIADADYQKGIIDCVICR	60	
OY	61	IPKEGGLSEFWEGCNLANVYRYFPQTQALNFAFKDKXKQLDFLGVDVDRHKQDFWRPFAGNIASG	120	

[illegible]

RESULT 9
S31935
ADP/ATP carrier protein - African malaria mosquito
C:Species: Anopheles gambiae (African malaria mosquito)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S31935; S31936
R:Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
;Reference number: S31935

A:Accession:S31935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BE>
A:Cross-references: EMBL:Z21814; EMBL:Z21815
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACPI>
F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:205-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match	73.68;	Score 1142.5;	DB 1;	Length 301;
Best Local Similarity	76.28;	Pred. NO. 6e-96;		
Matches 221; Conservative	26;	Mismatches 42;	Indels 1;	Gaps 1;

```
Oy      6 WSLKDFLAGAANAASVTAVAPIERVKLLIQVHASKQISAERKYKGIIIDCVRIPIKEQ 65
       : | ||||| ::||||||| ||||| : |||||::| |||||
Db      8 YGFANDELAGISAAVSSTAAPIERVKLLIQVAASKQIAVDKQYKGIYDCFVRIPKEQ 67
```

```
Oy      66 GFLSTWRGNLANVIRYPTQALNFAFKDKYKQLDLGVDRBHKOFMRYEAGNIASGGAAGA 125
        | :| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      68 GIGAFCCGGNLANVIRYPTQALNFAFKDYKYQVFLGVDRNTQFMRYEFLGNLGS GGGAAGA 127
```

QY 126 TSLCFVYPLDFARTRLADVGARA-QREHGLGDCIIFKSDGLRGLYGFNNVSGII 184
 ||||||| ||||| | : ||||: || | : ||||: ||||| |||||
 Db 128 TSLCFVYPLDFARTRLGADVGCAGEREFNGLDCLKTKTVKSDGIIGLYRGFNVSOGII 187

QY 185 IYRAYFGVYDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSYFPDTVRRRMMSGRK 244
 ||||| :||||||| ||||| ||| || :||:|||||||
 Db 188 IYRAYFGCEFTAKGMLPDPKNSTFVSMIAQSVTAAVTTASITSYPDTVRRRMMSGDC 247

QY 245 GADIMYTGIVDCWRKIAKDEGAKAFKKAWSNVLRGMGAFLVLVLYDEIK 294
:::| | :||| | | : ||||| :||| | | | :||| :
Db 248 KSEVMYKNITDCWVKIGKQEGSGAFFKGAFSNVLRGTGGALLVLVFYDEVK 297

RESULT 10
T25850
hypothetical protein T01B1.4 - *Caenorhabditis elegans*

C:\Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:\Accession: T25850
R:\celsel, C.; Stellyes, L.

A/Description: The sequence of C. elegans cosmid T01B1.
A/Reference number: Z20099
A/Accession: T25850

A: Molecule type: DNA
A: Residues: 1-313 <GEI>
A: Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4

A:Experimental source: SRIALIN BILSLOI NZ, CLOVE IVBIL
C:Genetics:
A:Gene: CESP:T01B11.4
A:Map position: 4

A:introns: 4/1; 191/2
C:superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match	67.3%;	Score 1045.5;	DB 2;	Length 313;
Best Local Similarity	69.8%;	Pred. No. 3.8e-87;		
Matches 203;	Conservative 36;	Mismatches 49;	Indels 3;	Gaps .2

```

Qy      8 FLKDELGAVAAAASVKTAAVAPLERVKLLQVQHAASKQISAEKQYKCIIDCVVRIPKEGEF 67
        ||| :| ||||| ||||| ||||| ||| :| :| ||||| :| :| ||||| :
Db      25 FLIDLASGGRAAASVKTAAVAPLERVKLLQVQDASLTIIADKRYKCIIVDVLVVRPKREGY 84

```

```

Qy      68  LSFMEGNLANVIRYPTQALNFAFKDKKQLFLGCVDRHKOFRWRYAGNLASGGAAGATS 1277
      : |||||
      85  AALMAGNLANVIRYPTQALNFAFKDKTKNIFQKGLDKKDKDFWKFPAAGNLASGGAAGATS 1444
Db

```

QY 128 LCFVYPLDFARTRLADVGRRAQREFHGLGDCITIKFKSDGLRGLYQGFNVSVQGITIYR 187

Db	145	LCFVYLPDFAFTRLAADVDGKANEDEFKGLADCLYKIAKSDPITGLYKGFVSYOGIIITR	204
Qy	188	AAYFGVYDPTAKGML-PDGRNVHIEVSWMIAOSVTAAGLSTSPEDTVRRRRMMOSGRGA	246
Db	205	AAYFGMEPTAKMVFADQKILNFFAAMVIAQVYVSGSILSTPYDTVRRRRMMOSGRK--	262
Qy	247	DIIMTGVYDCKMRKTAIDGGAFAAFKRGANSNVLBRMGCAFVLYLDELTKKYV	297
Db	263	DVLKNTLIDCAVKIITKNEGMSAMRGALSTNVEKGTGGLVLAITYDELQKIT	313

RESULT 11
T23207
hypothetical protein K01H12.2 - *Caenorhabditis elegans*

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C/Accession: T23207
R/McMurray, A.

A:Reference number: Z19707
A:Accession: T23207
A:Status: preliminary; translated from GB/EML/DBJ

A:Residues: 1-313 <MIL>
A:Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2
A:Experimental source: clone K01H12

C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A::Introns: 4/1, 191/2

Query Match	67.28;	Score	1043.5;	DB 2;	Length	313;
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[illegible]

68 LSFWRGNLANVIRYFP¹⁰QALNFAFKDKYKQ²⁰FLGCVDRH³⁰KQFWRYFAGNLASGGA⁴⁰ATS 127

Qy 128 LCFVVPIDFARTRLADVGRRAOREFHGJGDCIIKFKSDGLRGLYOGFNVSVOGIITVR 187

188 AAFPGVYDTAKGL-
PDPKNVHIFVSMIAQSYAVAGLLSTYPFDVRRMMQSGRGA 246

247 DIMYTGTVDCMKRIAKDEGAKAEFFKGAANSVLRCMGAFVLYLDEIKKYV 297

DB 263 DVLXNNTLDDCAVKRIINNEGMSAMEKGAISNVFRGTCGALVLAIDYDIQKFI 313

T25371
hypothetical protein T27E9.1 - *Caenorhabditis elegans*
0:Species: *Caenorhabditis elegans*

C/Accession: T25371
R; Lloyd, C.
submitted to the EMBL Data Library, November 1996

A:Accession: T25371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA

A:residues: 1-300 <MIL>
A:Cross-references: EMBL:Z82059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1

F:6-102/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACP3>

```
Query Match          58.2%; Score 904.5; DB 2; Length 301;
Best Local Similarity 58.3%; Pred. No. 2,2e-74;
Matches 172; Conservative 48; Mismatches 70; Indels 5; Gaps 4;

QY 7 SFLKDLGAVAAVAAVSKTAVAPIERVKLLIQVQHASKQISA--EKQYKGIIDCVRIPIKE 64
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 8 NFAADFLMGISAIKSTVVTPIERVKMLIQTDISIPIKSGOVERYSGLINCFKRVSK 67

QY 65 QGFLSPFNRGNLANVIRYFTQALNFAFKDKYKOLFLGVDVRHKOFWRYFAGNLASGGAAG 124
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 68 QGVLSLMRGNAVAVIRYFTQAFNFAKDYFKNIF--PRYDQNTDFSKFPCVNILSGATAG 126

QY 125 ATSLCFVYPLDFARTRLADVGRRARQREFHGLDCIIRKPSDGLRGLYOGFNVSVOGII 184
   ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 127 AISLLIVYPLDFARTRLASDVGKDRQFTGLFDCLAKIYKOTGLSLYSFGFVSVTGII 186

QY 185 IYRAATEGYVDTKKML-PDPKRVHIFVSMIAOSTAVAGLLSYEDTYRRRMMQSGR 243
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 187 VYRGSYFGLYDSAKALLFTNDKNTNIVLKWAAVQSVTIIAGLISYPEDTVRRRMMMSGR 246

QY 244 KG-ADIMYTGTVDCWRRIAKDEGAKAFPGKAGSNVLRGMGAFVLVLYDEIRKRV 297
   || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 247 KGEETIQYKNTIDCWIKILRNEGFKGFFGKAGMANVIRGAGALVLYFYDELQKLI 301
```

Search completed: February 13, 2002, 09:32:07
Job time: 44 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2002, 09:31:23 ; Search time 57.26 Seconds
(without alignments)
384.208 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDAWSEFLDLFLAGAVAA.....LRKGAFVLVLYDEIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: A.Geneseq_1101: *
2: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT: *
3: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT: *
4: /SID8/gcgdata/geneseq/geneseq/AA1982.DAT: *
5: /SID8/gcgdata/geneseq/geneseq/AA1983.DAT: *
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20: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT: *
21: /SID8/gcgdata/geneseq/geneseq/AA1999.DAT: *
22: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1553	100.0	297	21	AAV71031 Human adenine nucl
2	1553	100.0	297	22	AAU01198 Human adenine nucl
3	1457.5	93.9	298	19	AAW61169 Ant1 protein. Mus
4	1391.5	89.6	298	21	AAV71032 Human adenine nucl
5	1391.5	89.6	298	22	AAU01199 Human adenine nucl
6	1385.5	89.2	298	21	AAV71033 Human adenine nucl
7	1385.5	89.2	298	22	AAW39641 Human polypeptide
8	1385.5	89.2	298	22	AAU01200 Human adenine nucl
9	1385.5	89.2	323	22	AAW41427 Human polypeptide
10	746	48.0	346	21	AAW36577 Arabidopsis thalia
11	746	48.0	346	21	AAW37261 Arabidopsis thalia

12	746	48.0	346	21	AAW37264 Arabidopsis thalia
13	746	48.0	346	21	AAW38460 Arabidopsis thalia
14	746	48.0	363	21	AAW36576 Arabidopsis thalia
15	746	48.0	363	21	AAW37260 Arabidopsis thalia
16	746	48.0	363	21	AAW37263 Arabidopsis thalia
17	746	48.0	363	21	AAW38459 Arabidopsis thalia
18	746	48.0	381	21	AAW36575 Arabidopsis thalia
19	746	48.0	381	21	AAW37259 Arabidopsis thalia
20	746	48.0	381	21	AAW37262 Arabidopsis thalia
21	746	48.0	381	21	AAW38458 Arabidopsis thalia
22	746	48.0	992	21	AAW38672 Arabidopsis thalia
23	746	48.0	1009	21	AAW38671 Arabidopsis thalia
24	746	48.0	1027	21	AAW38670 Arabidopsis thalia
25	743	47.8	346	21	AAW17731 Arabidopsis thalia
26	743	47.8	363	21	AAW17730 Arabidopsis thalia
27	743	47.8	381	21	AAW17729 Arabidopsis thalia
28	734	47.3	386	22	AAW00106 ADP/ATP carrier pr
29	686	44.2	333	21	AAW06857 Arabidopsis thalia
30	686	44.2	350	21	AAW06856 Arabidopsis thalia
31	686	44.2	368	21	AAW06855 Arabidopsis thalia
32	682	43.9	330	21	AAW20658 Arabidopsis thalia
33	681	43.9	330	21	AAW39398 Arabidopsis thalia
34	651.5	42.0	306	21	AAW12916 Arabidopsis thalia
35	651.5	42.0	306	21	AAW16974 Arabidopsis thalia
36	646	41.6	291	21	AAW20659 Arabidopsis thalia
37	645	41.5	291	21	AAW39399 Arabidopsis thalia
38	636.5	41.0	291	21	AAW12917 Arabidopsis thalia
39	636.5	41.0	291	21	AAW16975 Arabidopsis thalia
40	577	37.2	249	21	AAW20660 Arabidopsis thalia
41	576	37.1	249	21	AAW39400 Arabidopsis thalia
42	574	37.0	263	21	AAW12918 Arabidopsis thalia
43	574	37.0	263	21	AAW16976 Arabidopsis thalia
44	570	36.7	312	21	AAW28188 Arabidopsis thalia
45	557	35.9	228	21	AAW28189 Arabidopsis thalia

ALIGNMENTS

RESULT 1	
AAV71031	AAV71031 standard; Protein; 297 AA.
XX	
AC	AAV71031:
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Human adenine nucleotide translocator ANTL.
KW	Human: adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP;
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotropic;
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW	antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIND;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	
OS	Homo sapiens.
XX	
PN	W0200026370-A2.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99MO-US25883.
XX	
PR	03-NOV-1998; 98US-0185904.
XX	
PR	08-SEP-1999; 99US-0393441.
XX	
XX	(MITO-) MITOKOR.
XX	

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR MPI: 2000-365619/31.
 DR N-PSDB: AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX
 PS Claim 44; Page 172; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANTI from human brain.
 XX
 SQ Sequence 297 AA:
 100.0%; Score 1553; DB 21; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1.3e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGIIIDCVR 60
 DB 1 mgdhmsflkdfllagaaaavsktavapiervklllyqhaskqsaekygiidcvr 60
 QY 61 IPKEGFLSFWMGNLANYIRFPTQALNFAFKDKYKQFLGVDVDRHKQFWRFAAGNLASG 120
 DB 61 ipkegflsftwgnlanvlyrfptqalnfaefkdkyqflfgvdrhkqfwrfaagnlasg 120
 QY 121 GAAGATSLCFVPLDFARTRLADYGRRAQREFHGLDCIIRFKSDGLRGLYOGFNNVS 180
 DB 121 gaagatslcfvpldfartrladvgrraqrrefhglgdcilrkfsdglrglyogfnnvs 180
 QY 181 OGIIIRAAVFGVYDTAKGMLPDPKNNHIFVSWMTAQSVTAVAGLSYPTDVRRRMMQ 240
 DB 181 ogiirraavfgvydtakgmlpdpknnhlfvswmtaqsvtavaglsyptdvrrrmmq 240
 QY 241 SGRKGADIWYTGTCVCRKRIADKDEGAKAFKGAWSNVLRGMSGAFVLYLYDEIKRYV 297
 DB 241 sgrkgadimwgtvcwrkiaekgakaflkgawsnvlrmsgafvlylydeikryv 297

RESULT 2
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX
 AC AAU01198;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX
 KW Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX

OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Fritzer LG;
 PI Vellacelebl G, Davis RE;
 DR MPI: 2001-291054/30.
 DR N-PSDB: AAS05901.
 XX
 CC New nucleic acid expression constructs, useful for screening for agents
 CC that alter mitochondrial permeability transition (MPT), comprises
 CC polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 CC fused to energy transfer molecule -
 XX
 PS Disclosure: Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 297 AA:
 100.0%; Score 1553; DB 22; Length 297;
 Best Local Similarity 100.0%; Pred. No. 1.3e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGIIIDCVR 60
 DB 1 mgdhmsflkdfllagaaaavsktavapiervklllyqhaskqsaekygiidcvr 60
 QY 61 IPKEGFLSFWMGNLANYIRFPTQALNFAFKDKYKQFLGVDVDRHKQFWRFAAGNLASG 120
 DB 61 ipkegflsftwgnlanvlyrfptqalnfaefkdkyqflfgvdrhkqfwrfaagnlasg 120
 QY 121 GAAGATSLCFVPLDFARTRLADYGRRAQREFHGLDCIIRFKSDGLRGLYOGFNNVS 180
 DB 121 gaagatslcfvpldfartrladvgrraqrrefhglgdcilrkfsdglrglyogfnnvs 180
 QY 181 OGIIIRAAVFGVYDTAKGMLPDPKNNHIFVSWMTAQSVTAVAGLSYPTDVRRRMMQ 240
 DB 181 ogiirraavfgvydtakgmlpdpknnhlfvswmtaqsvtavaglsyptdvrrrmmq 240
 QY 241 SGRKGADIWYTGTCVCRKRIADKDEGAKAFKGAWSNVLRGMSGAFVLYLYDEIKRYV 297
 DB 241 sgrkgadimwgtvcwrkiaekgakaflkgawsnvlrmsgafvlylydeikryv 297

RESULT 3
AAW61169 standard; Protein: 298 AA.
ID AAW61169 standard; Protein: 298 AA.
AC AAW61169;
XX
XX 28-SEP-1998 (first entry)
XX
XX
XX Ant1 protein.
XX
XX Ant1. Adenine nucleotide translocator; cloning; screening;
XX DNA Tag di-deoxy terminator cycle sequencing; oxidative phosphorylation;
XX probe; OXPHOS; mitochondrial; ADP; ATP; homozygous mutant; myopathy;
XX hypertrophic cardiomyopathy; fasciocalcular humeral muscular dystrophy;
XX lactic acidosis; degenerative muscle disease.
XX
XX Mus sp.
XX
XX WO9819714-A1.
XX
XX 14-MAY-1998.
XX
XX 31-OCT-1997; 97WO-US19882.
XX
XX 01-NOV-1996; 96US-0030017.
XX
XX (UYEM-) UNIV EMORY.
XX
XX Graham BC, Macgregor GR, Wallace DC;
XX
XX WPI; 1998-286608/25.
XX
XX N-PSDB; AAV36479.
XX
XX Mice lacking heart-muscle adenine nucleotide translocator protein -
XX useful as model for mitochondrial myopathy and hypertrophic
XX cardiomyopathy in animals and to test therapeutic compositions or
XX gene therapies
XX
XX
XX Disclosure: Page 39-40; 61pp; English.
XX
XX The present sequence is the mouse Ant1 protein, the cDNA producing this
XX polypeptide is cloned by screening a mouse heart cDNA library with the
XX human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA
XX Tag di-deoxy terminator cycle sequencing. The Ant1 protein is encoded by
XX the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
XX in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
XX which can then be converted into ATP. An Ant1 homozygous mutant would
XX thus be defective in OXPHOS which results in disease in oxidative
XX metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
XX used as a model system for fasciocalcular humeral muscular dystrophy,
XX hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
XX systems can be used to test possible therapeutic compounds which
XX increase/mediate ATP and ADP exchange across the mitochondrial membrane
XX independent of Ant1.
XX
XX
XX Sequence 298 AA:
SQ
Query Match 93.9%; Score 1457.5; DB 19; Length 298;
Best Local Similarity 93.6%; Pred. No. 2.2e-162;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
OY 1 MGDHAWFLDPLAGAAVAVSKTAVAPTRERVKLLLOVQHAOSIASEKQKGLTDCVVR 60
Db 1 mgddaisflkdfllagglaaavsktavaplerVKLLlqvqnskqisEEKgkglldcvvr 60
OY 1 PKBQGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHMQFWRYFAGNLASG 120
Db 1 kpegqglstfvrqnlavirlyfpcgalnfakdkykgllfvgvdrhmqfwryfagnlasg 120
OY 121 GAAGATSLCFYPLDFAFTRLAADVGR-RAQREHGLGDCITIKFKSDGLGLYQGRNVS 179
Db 121 gaagatslctfypldfartlaadvgrkysqgrefngldcltklfsdgjkglyvgfsvs 180

OY 180 VQGITIYRAAFGVYDTRAKGMLPDPKNNHIFVSMIAOSYAVAGLSYPEDTVRRBM 239
Db 181 vqgilliyraafigvyddakgnldpdknvhilvswlqagvavaglysyptdvttrrrmm 240
OY 240 QSGRRGADIMYTGTVDCWRKIAKDEGAKAFKAGMSVNLRCMGAFVLYLDEIKKYV 297
Db 241 qsgrrgadimlytgldcwrklakdeganaffkgawmsvnlrgmgafvlylydelkkyv 298
RESULT 4
AAV71032 standard; Protein: 298 AA.
ID AAV71032 standard; Protein: 298 AA.
XX
XX AAV71032;
XX
XX 29-AUG-2000 (first entry)
XX
XX
XX Human adenine nucleotide translocator ANT2.
XX
XX
XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
XX adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
XX mitochondrial permeability transition; neuroprotective; noctropic;
XX antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
XX antipariatic; cerebroprotective; therapeutic; screening; psoriasis;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
XX diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
XX mitochondrial encephalopathy; lactic acidosis; stroke; MIDO;
XX myoclonic epilepsy red ragged fibre syndrome.
XX
XX Homo sapiens.
XX
XX
XX WO200026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25883.
XX
XX 03-NOV-1998; 98US-0185904.
XX
XX 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.
XX
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
XX Ghosh SS;
XX
XX WPI; 2000-365619/31.
XX
XX N-PSDB; AAD00520.
XX
XX
XX Recombinant construct encoding adenine nucleotide translocator
XX polypeptide, useful e.g. in screening for potential therapeutic agents
XX against mitochondrial disease
XX
XX
XX
XX Claim 45; Page 172-173; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
XX (ANT) proteins or ANT fusion proteins using recombinant expression
XX constructs. ANT is a nuclear encoded protein and a major component of
XX inner mitochondrial membrane. It mediates transport of adenosine
XX di/tri-phosphates across the mitochondrial inner membrane and also serves
XX as an important molecular component of the mitochondrial permeability
XX transition pore, a modulator of apoptosis. ANT is used to identify agents
XX or ligands that bind to, or interact with it. The ANT ligands are used to
XX detect or isolate ANT in a biological sample, and therapeutically for
XX regulating mitochondrial pore activity, for treating diseases associated
XX with altered mitochondrial function, including Alzheimer's, Parkinson's
XX and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
XX Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
XX encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
XX disorders, mitochondrial diabetes and deafness (MIDO), and myoclonic
XX epilepsy red ragged fibre syndrome. The present sequence is an
XX adenine nucleotide translocator ANT2 from human brain.

```

XX      Sequence      298 AA:
SQ
Query Match      89.6%; Score 1391.5; DB 21; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.2e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY      1 MGDHANSFLKDFLAGAANAASVTAVAPIERVKLLQVGHASKQISAERQYGIIDCVYR 60
      1 mtdaaistfakdfilagvaaaistavapiervklllqvghaskqiladkqygidcvvr 60
DB
OY      61 IREQGFLEFWMGNLANVIRYPTQALNFAFKDKYKQLGLGVDRKHQWRFRAGNLASG 120
      61 ipekegevlstfwgnlanviryptqalnfafrkdkykqlglgvdrkhqwrfragnlasg 120
DB
OY      121 GAAGATSLCFVYPLDFARFRLADVGR--AOREFHGLGDCIIRFKSDGLRGLYOGFNV 179
      121 gaagatslcfvypldfartcrlaadvgkagaerefrlgdclvkiysdglklyggnvns 180
DB
OY      180 VOGIITRYAAREGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYPFDRRRMM 239
      181 vggililyraayfigyldakgmldpdknthlvswmlaqsvtavagllsyfpdtrrrmm 240
DB
OY      240 QSGRKADIMYTGTVDCMKRIADGAKAFKFGAMSNVLRMGAGFVLYLYDEIKKY 296
      241 qsgrkadimytgtvdcmrkriadegakafkfgawsnvlrmgagfvlvlydeikky 297
DB

RESULT 5
AAU01199
ID      AAU01199 standard; Protein; 298 AA.
AC
AC      AAU01199;
XX
XX      07-SEP-2001 (first entry)
DE      Human adenine nucleotide translocator-2 (ANT-2) protein.
XX
XX      Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
KW      mitochondrial permeability transition pore component; cell survival;
KW      mitochondrial core component; mitochondrial related disorder; cancer;
KW      Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX
OS      Homo sapiens.
XX
XX      WO200132876-A2.
XX
XX      10-MAY-2001.
XX
XX      03-NOV-2000; 2000MO-US30535.
XX
XX      03-NOV-1999; 99US-0434354.
XX
XX      (MITO-) MITOKOR.
XX
XX      Murphy AN, Cleveneger W, Wiley SE, Andreyev AY, Frigeri LG;
PI      Velicelebi G, Davis RE;
XX
XX      WPI; 2001-291054/30.
XX
XX      N-PSDB; AAS05902.
XX
XX      New nucleic acid expression constructs, useful for screening for agents
PT      that alter mitochondrial permeability transition (MPT), comprises
PT      polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT      fused to energy transfer molecule -
XX
XX
PS      Disclosure; Fig 2; 186pp; English.
XX
XX      The present sequence represents human adenine nucleotide translocator-2
CC      (ANT-2) protein. ANT proteins are mitochondrial permeability
CC      transition (MPT) pore components responsible for mediating transport.
CC      of ADP across the mitochondrial inner membrane. ANT proteins interact

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CC      with other mitochondrial core components e.g. cyclophilins to
CC      regulate MPT. The present invention relates to a novel nucleic acid
CC      expression construct comprising a promoter operably linked to a
CC      polynucleotide encoding a mitochondrial pore component polypeptide
CC      (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC      (e.g. green fluorescent protein (GFP) or a FLASh sequence). The novel
CC      expression construct can alter mitochondrial membrane permeability
CC      transition and/or alter the interaction between mitochondrial core
CC      components. The methods are useful for screening for agents that alter
CC      MPT and/or cell survival. These agents are useful for the prevention or
CC      treatment of diseases associated with altered mitochondrial function or
CC      dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC      mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC      mitochondrial encephalopathy, lactic acidosis, stroke,
CC      hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ      Sequence      298 AA:
Query Match      89.6%; Score 1391.5; DB 22; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.2e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY      1 MGDHANSFLKDFLAGAANAASVTAVAPIERVKLLQVGHASKQISAERQYGIIDCVYR 60
      1 mtdaaistfakdfilagvaaaistavapiervklllqvghaskqiladkqygidcvvr 60
DB
OY      61 IREQGFLEFWMGNLANVIRYPTQALNFAFKDKYKQLGLGVDRKHQWRFRAGNLASG 120
      61 ipekegevlstfwgnlanviryptqalnfafrkdkykqlglgvdrkhqwrfragnlasg 120
DB
OY      121 GAAGATSLCFVYPLDFARFRLADVGR--AOREFHGLGDCIIRFKSDGLRGLYOGFNV 179
      121 gaagatslcfvypldfartcrlaadvgkagaerefrlgdclvkiysdglklyggnvns 180
DB
OY      180 VOGIITRYAAREGVYDTAKGMLPDPKNVHIFVSWMLAQSVTAVAGLLSYPFDRRRMM 239
      181 vggililyraayfigyldakgmldpdknthlvswmlaqsvtavagllsyfpdtrrrmm 240
DB
OY      240 QSGRKADIMYTGTVDCMKRIADGAKAFKFGAMSNVLRMGAGFVLYLYDEIKKY 296
      241 qsgrkadimytgtvdcmrkriadegakafkfgawsnvlrmgagfvlvlydeikky 297
DB

RESULT 6
AA71033
ID      AA71033 standard; Protein; 298 AA.
AC
AC      AA71033;
XX
XX      29-AUG-2000 (first entry)
DE      Human adenine nucleotide translocator ANT3.
XX
XX      Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW      adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW      mitochondrial permeability transition; neuroprotective; noctoptic;
KW      antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW      antipsoriatic; cerebroprotective; therapeutic; psoriasis;
KW      Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW      diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW      mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW      mitochondrial diabetes and deafness; hyperproliferative disorder;
KW      myoclonic epilepsy red ragged fibre syndrome.
XX
XX
OS      Homo sapiens.
XX
XX      WO2000026370-A2.
XX
XX      11-MAY-2000.
XX
XX      03-NOV-1999; 99MO-US25883.
XX

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QY 180 VGGIIIRAAFGVYDTAKGMLPDPKNNHIFVSWMIAOSVTAAGLSYPTVRRMM 239
 |||||||
 Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNNHIFVSWMIAOSVTAAGLSYPTVRRMM 240
 |||||||

QY 240 OSGRGADIMYGTVDCKWRIKDEGAKAFKAGMSNVLRGAGAFVLYLDEIRKYV 297
 |||||||
 Db 241 GSGRGADIMYGTVDCKWRIKDEGAKAFKAGMSNVLRGAGAFVLYLDEIRKYV 298
 |||||||

RESULT 8

ID AAM01200 standard: Protein; 298 AA.

AC AAM01200;

DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-3 (ANT-3) protein.

XX Human; adenine nucleotide translocator-3; ANT-3; MPT; cyclophilin;

KM mitochondrial permeability transition pore component; cell survival;

KM mitochondrial core component; mitochondrial related disorder; cancer;

KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX Homo sapiens.

XX WO200132876-A2.

XX 10-MAY-2001.

XX 03-NOV-2000; 2000WO-US30535.

XX 03-NOV-1999; 99US-0434354.

XX (MITO-) MITOKOR.

XX Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritgeri LG;

XX Vellceleb G, Davis RE;

XX WPI; 2001-291054/30.

XX N-PSDB; AAS05903.

XX New nucleic acid expression constructs, useful for screening for agents

XX that alter mitochondrial permeability transition (MPT), comprises

XX polynucleotide encoding MPT polypeptide or cyclophilin polypeptide

XX fused to energy transfer molecule -

XX Disclosure; Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-3

XX (ANT-3) protein. ANT proteins are mitochondrial permeability

XX transition (MPT) pore components responsible for mediating transport

XX of ADP across the mitochondrial inner membrane. ANT proteins interact

XX with other mitochondrial core components e.g. cyclophilins to

XX regulate MPT. The present invention relates to a novel nucleic acid

XX expression construct comprising a promoter operably linked to a

XX polynucleotide encoding a mitochondrial pore component polypeptide

XX (e.g. ANT) fused to an energy transfer molecule (ETM) protein

XX (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel

Query Match 89.2%; Score 1385.5; DB 22; Length 298;

Best local similarity 87.2%; Pred. No. 6.1e-154;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPTERKLLLOVQHASKOISAEKQYGIIDCYVR 60

Db 1 MEGASISTAKDLIAGLIAAIAISKAVAPLERVKLLIQVHASKGIAADQYKGYVDCIVR 60

QY 61 IPKEGFLSFMRGNLANVRYRPTOALNFAKFKKQKOLEGLGVDVRRHKKFWRFAAGNLASG 120

Db 61 IPKEGFLSFMRGNLANVRYRPTOALNFAKFKKQKOLEGLGVDVRRHKKFWRFAAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLGDCIIRKISDGLKGLYGFNV 179

Db 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLGDCIIRKISDGLKGLYGFNV 179

QY 180 VGGIIIRAAFGVYDTAKGMLPDPKNNHIFVSWMIAOSVTAAGLSYPTVRRMM 239

Db 181 VGGIIIRAAFGVYDTAKGMLPDPKNNHIFVSWMIAOSVTAAGLSYPTVRRMM 240

QY 240 OSGRGADIMYGTVDCKWRIKDEGAKAFKAGMSNVLRGAGAFVLYLDEIRKYV 297

Db 241 GSGRGADIMYGTVDCKWRIKDEGAKAFKAGMSNVLRGAGAFVLYLDEIRKYV 298

RESULT 9

ID AAM41427 standard: Protein; 323 AA.

AC AAM41427;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6358.

XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;

KM peripheral nervous system; neuropathy; central nervous system; CNS;

KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KM chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

XX Leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSE INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao Qa, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

XX N-PSDB; AA160583.

XX Novel nucleic acids and polypeptides, useful for treating disorders

XX such as central nervous system injuries -

XX Example 2; SEQ ID NO 6358; 10078pp; English.

CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA038642-AA042213) with neurotropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 323 AA;

Query Match	89.28;	Score 1385.5;	DB 22;	Length 323;
Best Local Similarity	87.28;	Pred..No. 6.8e-154;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 14

Oy	1	MGDHAAFEELKDFLGAAGAAAASKRPAVPIRRVKLLLOVDHASKOISAEKKOYLICDVR	60
Dd	26	mteqajstafkdflagjdaaastkavapjerlvlllqvgnasqjaadckykajivdcivr	85
Oy	61	IPKEQGFLEWKGMLANVIRYPTQALNFAFKDKYKOLPLGVDNRHKOFMYEAGNLASG	120
Dd	86	lpkeqgvlsfwrgnlavlivyfrpcqanfaikdkkykfllgvdkhngfwvrlfagnlasg	145
Oy	121	GAAATSLSCFFYRPLDFAFRTLRGAADVGR-AORENHGSGDCILIKTFKSDGLRGLOGNVS	179
Dd	146	gaagatsctlyrpdifartcilaadvsgsferefrlgdcvlwtkxsdglrtglvgysvs	205
Oy	180	VQGIIIRYAAYFGVYDPAKGMLPDPKVVHHIFVSMIAIOSVTAAAGLSYPEDIVRRMM	239
Dd	206	vqgilliyraayfyuyldcakgmllpprrnthilvsmmlaqvtvatavgvsvpfcdetvrrmm	265
Oy	240	QSGRKGGADIMTGTVCDCWRKTAAKDEGAKAFPGAMSVLRMGAGAPVLVLYDEIKTV	297
	266	gsqgtkggdlimtgcvcdwcrklftdeegkaefkawsnvlrgmgafalvlydgelkkvi	323

RESULT	10
AAG36577	
ID	AAG36577 standard; Protein; 346 AA.

AC MAG36577;

DT 18-OCT-2000 (flrst entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 44845.

KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.

PR 09-MAR-1999; 99US-0123548.

PR 25-MAR-1999; 99US-0126264

PR	01- AAR -1999	9905-0127462
PR	06- AAR -1999	9905-0128234
PR	08- AAR -1999	9905-0128714
PR	16- AAR -1999	9905-0129845
PR	19- AAR -1999	9905-0130077
PR	21- AAR -1999	9905-0130449
PR	22- AAR -1999	9905-0130591
PR	28- AAR -1999	9905-0131449
PR	30- AAR -1999	9905-0132048
PR	04- AAR -1999	9905-0132407
PR	04- MAY -1999	9905-0132484
PR	05- MAY -1999	9905-0132485
PR	06- MAY -1999	9905-0133246
PR	05- MAY -1999	9905-0132487
PR	07- MAY -1999	9905-0132863
PR	11- MAY -1999	9905-0134256
PR	14- MAY -1999	9905-0134218
PR	14- MAY -1999	9905-0134219
PR	14- MAY -1999	9905-0134370
PR	18- MAY -1999	9905-0134768
PR	13- MAY -1999	9905-0135124
PR	20- MAY -1999	9905-0135194
PR	21- MAY -1999	9905-0135353
PR	24- MAY -1999	9905-0135629
PR	25- MAY -1999	9905-0136392
PR	27- MAY -1999	9905-0136501
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DB 161 gassllrvysldyartlandakaakakgsggrqIdglvdyvyrklktIdglaglyrftnls 220
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DB 221 cvglIivrglyfgyldsvkpylltgdlqd---sfasfalgwltngaglsypIdtvr 276
OY 235 RRMAMOSGRKADIMYTGTVDPCWRIAKDEGAKAFKGAWSNVLRGMGARVLYIDEI- 293
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XX AAG37261;

DT 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SRO ID NO: 45788.

KW protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

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XX	Protein identification; signal transduction pathway; metabolic pathway;		
XX	hybridisation assay; genetic mapping; gene expression control; promoter;		
XX	termination sequence.		
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XX 18-OCT-2000 (first entry)
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XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 45787.

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

OS *Arabidopsis thaliana*.

PN EP1033405-A2.

PD 06-SEP-2000.

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Best Local Similarity 53.9%; Pred. No. 8.5e-79;

Matches 166; Conservative 39; Mismatches 75; Indels 28; Gaps 8;

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Search completed: February 13, 2002, 09:33:11
Job time: 108 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:34:14 ; Search time 55.37 Seconds
(without alignments)
787.234 Million cell updates/sec

Title: US-09-393-441-32
Perfect score: 1547
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Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
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10: sp.plant:*
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13: sp.vertibrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1446	93.5	298	13	O9PRH1
2	1443	93.3	298	13	O9PRH2
3	1439	93.0	298	13	O9YIC4
4	1435	92.1	298	13	O919M9
5	1423	92.0	298	6	O46373
6	1417	91.6	298	11	O62164
7	1295	83.7	317	13	O91336
8	1248.5	80.7	300	5	O9NHWS
9	1190.5	77.0	288	5	O44093
10	1185.5	76.6	288	5	O44094
11	1145.5	74.0	304	5	O25129
12	1125.5	72.8	307	5	O62526
13	1102	71.2	315	4	O9HOC2
14	1032	66.7	300	5	O45865
15	1029	66.5	313	5	P91410
16	1029	66.5	313	5	O21103
17	986	63.7	300	5	O01813
18	985	63.7	309	5	O97470
19	983	63.5	300	5	O17407

20	950.5	61.4	318	5	O9BU36	O9b136 toxoplasma
21	949.5	61.4	307	8	O9XM22	O9xm22 ascaris suu
22	939	60.7	301	5	O25692	O25692 plasmodium
23	938	60.6	301	5	O26006	O26006 plasmodium
24	819	52.9	170	6	O9XS69	O9xs69 sus scrofa
25	778	50.3	305	3	O9P8M1	O9p8m1 yarrowia ll
26	759	49.1	326	5	P91270	P91270 caenorhabdi
27	755	48.8	303	3	O74260	O74260 candida par
28	753.5	48.7	385	10	O9FY52	O9fy52 arabidopsis
29	753	48.7	317	5	O9N647	O9n647 leishmania
30	752	48.6	307	5	O76286	O76286 trypanosoma
31	750	48.5	386	10	P93767	P93767 lycopersico
32	749.5	48.4	306	5	O18683	O18683 caenorhabdi
33	747	48.3	388	10	O49875	O49875 lupinus alb
34	746	48.2	306	3	P78754	P78754 schizosacch
35	746	48.2	379	10	O49447	O49447 arabidopsis
36	745	48.2	307	5	O26697	O26697 trypanosoma
37	740	47.8	331	10	O41628	O41628 tritlicum tu
38	721.5	46.6	305	3	O9P876	O9p876 pichia jadt
39	718.5	46.4	305	3	O9P875	O9p875 pichia jadt
40	690.5	44.6	330	10	O9FM86	O9fm86 arabidopsis
41	665.5	43.0	298	5	O21809	O21809 caenorhabdi
42	656.5	42.4	262	10	O9AVT6	O9avt6 picea abies
43	521.5	33.7	327	10	O9LF44	O9lf44 arabidopsis
44	509.5	32.9	162	5	O26130	O26130 plasmodium
45	447.5	28.9	158	5	O76467	O76467 heterodera

ALIGNMENTS

RESULT 1
ID O9PRH1 PRELIMINARY; PRT; 298 AA.
AC O9PRH1;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxId=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Mura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
Z, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998)
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -!- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008463; BAA36513.1; -;
DR EMBL: AB008456; BAA36506.1; -;
DR EMBL: AB008461; BAA36511.1; -;
DR EMBL: AB008462; BAA36512.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match 93.5% Score 1446; DB 13; Length 298;
Best Local Similarity 91.9%; Pred. No. 1,2e-121;
Matches 273; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKOTADKQYGIIDCVVR 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKOTADKQYGIIDCVVR 60
QY 61 IRKEQEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 IRKEQEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYSDGIKGLYGFNV 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYSDGIKGLYGFNV 180
QY 181 VOGIIIRAAAYGIDYDTAKGMLPDPKRNTHIVISWMIAGTVTAAGLTSYPTVRRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 VOGIIIRAAAYGIDYDTAKGMLPDPKRNTHIVISWMIAGTVTAAGLTSYPTVRRRMM 240
QY 241 OSGRKGTDIMYGTGLDCKRKIRADEGKAFKFGAMSNVLRGKGAFVLYLDEIKKY 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 OSGRKGAEIMYSGTIDCKMKIARDEGSRAFKFGAMSNVLRGKGAFVLYLDEIKKY 297

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RESULT 2

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Q9PRH2 PRELIMINARY: PRT: 298 AA.
ID O9PRH2
AC O9PRH2:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
RN NCBI_TaxID=8410;
RN [1]
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
CC EMBL: AB008460; BAA36510.1; -.
DR EMBL: AB008458; BAA36508.1; -.
DR EMBL: AB008459; BAA36509.1; -.
DR InterPro: IPR001993; Mitoch.carrier.
DR InterPro: IPR002067; Mit.carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr: 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH.CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA: 33082 MW; B0E225E867599A06 CRC64;

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Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 2.3e-121;
 Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKOTADKQYGIIDCVVR 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKOTADKQYGIIDCVVR 60
QY 61 IRKEQEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 IRKEQEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYSDGIKGLYGFNV 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYSDGIKGLYGFNV 180

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QY 181 VOGIIIRAAAYGIDYDTAKGMLPDPKRNTHIVISWMIAGTVTAAGLTSYPTVRRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 VOGIIIRAAAYGIDYDTAKGMLPDPKRNTHIVISWMIAGTVTAAGLTSYPTVRRRMM 240
QY 241 OSGRKGTDIMYGTGLDCKRKIRADEGKAFKFGAMSNVLRGKGAFVLYLDEIKKY 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 OSGRKGAEIMYSGTIDCKMKIARDEGSRAFKFGAMSNVLRGKGAFVLYLDEIKKY 297

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RESULT 3

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Q9YIC4 PRELIMINARY: PRT: 298 AA.
ID Q9YIC4
AC Q9YIC4:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DE 01-JUN-1999 (TREMBlrel. 10, Last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
RN NCBI_TaxID=8410;
RN [1]
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC EMBL: AB008457; BAA36507.1; -.
DR EMBL: AB008457; BAA36507.1; -.
DR InterPro: IPR001993; Mitoch.carrier.
DR InterPro: IPR002067; Mit.carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr: 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH.CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA: 33068 MW; 15B270ED37099A00 CRC64;

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Query Match 93.0%; Score 1439; DB 13; Length 298;
 Best Local Similarity 91.2%; Pred. No. 5.2e-121;
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

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QY 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKOTADKQYGIIDCVVR 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MTDALISFAKDLPLAGVAAAIKSTAVAPIERVKLLQVHASKOTADKQYGIIDCVVR 60
QY 61 IRKEQEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 IRKEQEVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVNDKRTQWRPFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYSDGIKGLYGFNV 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GAAGATSLCFVYPLDFARTRLADYVGKAGAREFRGLGDCLVKIKYSDGIKGLYGFNV 180
QY 181 VOGIIIRAAAYGIDYDTAKGMLPDPKRNTHIVISWMIAGTVTAAGLTSYPTVRRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 VOGIIIRAAAYGIDYDTAKGMLPDPKRNTHIVISWMIAGTVTAAGLTSYPTVRRRMM 240
QY 241 OSGRKGTDIMYGTGLDCKRKIRADEGKAFKFGAMSNVLRGKGAFVLYLDEIKKY 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 OSGRKGAEIMYSGTIDCKMKIARDEGSRAFKFGAMSNVLRGKGAFVLYLDEIKKY 297

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RESULT 4
 Q919M9 PRELIMINARY: PRT: 298 AA.

DR EMBL: AF240002; AAF64470.1; -
 DR EMBL: BC003791; AAH03791.1; -
 DR MGD: MGI:1353495; SLC25a4.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mltc_carrier.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 KW SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match 91.6%; Score 1417; DB 11; Length 298;
 Best Local Similarity 89.6%; Pred. No. 4.9e-119;

Matches 26; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSFADKDLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADQYKGIIDCVVR 60
 DB 1 MDDQALSFADKDLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADQYKGIIDCVVR 60
 QY 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFYAGNLASG 120
 DB 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFYAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLADYKAGAREFRGLDCLVYKSDIGKLYGQFNVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLADYKAGAREFRGLDCLVYKSDIGKLYGQFNVS 180
 QY 121 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGTSPPTVRRMM 240
 DB 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGTSPPTVRRMM 240
 DB 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGTSPPTVRRMM 240
 QY 241 OSGRKGTDMYTGTLDCWKRIARDEGKAFFKAGSNVLRGGAFAVLVYDEIKKY 297
 DB 241 OSGRKGTDMYTGTLDCWKRIARDEGKAFFKAGSNVLRGGAFAVLVYDEIKKY 297

RESULT 7

Q91336 PRELIMINARY; PRT; 317 AA.

AC Q91336
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ADP/ATP TRANSLUCASE.
 OS Rana sylvatica (wood frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
 CC NCBI_TaxId=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cai Q., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress";
 RL Biochim. Biophys. Acta 1353:69-78(1997).
 RN [2]
 RP REVISIONS.
 RA Cai Q., Storey K.B.;
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: U44832; AAA97882.2; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mltc_carrier.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SEQUENCE 317 AA; 35005 MW; 5F687EDBD5CEB72 CRC64;

Query Match 83.7%; Score 1295; DB 13; Length 317;
 Best Local Similarity 90.1%; Pred. No. 4.6e-108;
 Matches 245; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTDALSFADKDLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADQYKGIIDCVVR 60
 DB 1 MDDQALSFADKDLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADQYKGIIDCVVR 60
 QY 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFYAGNLASG 120
 DB 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFYAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLADYKAGAREFRGLDCLVYKSDIGKLYGQFNVS 180
 DB 121 GAAGATSLCFVYPLDPARTRLADYKAGAREFRGLDCLVYKSDIGKLYGQFNVS 180
 QY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGTSPPTVRRMM 240
 DB 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGTSPPTVRRMM 240
 QY 241 OSGRKGTDMYTGTLDCWKRIARDEGKAFFK 272
 DB 241 OSGRKGTDMYTGTLDCWKRIARDEGKAFFR 272

RESULT 8

Q9NHM5 PRELIMINARY; PRT; 300 AA.

AC Q9NHM5
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ADP/ATP TRANSLUCASE.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Oestroidea; Calliphoridae; Lucilia.
 CC NCBI_TaxId=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS MAL SEEKING;
 RA Chen Z., Fair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";
 RL Submitted (Dec-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC EMBL: AF218547; AAF32322.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mltc_carrier.
 DR PRINTS: PR00926; MITOCH_CARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SEQUENCE 300 AA; 33036 MW; 5459D0E0E2E742 CRC64;

Query Match 80.7%; Score 1248.5; DB 5; Length 300;
 Best Local Similarity 81.2%; Pred. No. 6.3e-104;
 Matches 237; Conservative 20; Mismatches 34; Indels 1; Gaps 1;

QY 6 LSFADKDLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADQYKGIIDCVVRIPKEQ 65
 DB 9 LGEVADKDLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADQYKGIIDCVVRIPKEQ 68
 QY 66 EYLSWGRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFYAGNLASGAAGA 125
 DB 69 GRASYWGRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFYAGNLASGAAGA 128
 QY 126 TSLCFVYPLDPARTRLADYKAGAREFRGLDCLVYKSDIGKLYGQFNVSVOGII 185,
 DB 129 TSLCFVYPLDPARTRLADYTK-GGOREFTGLGNCLAKIFNSDGLVGLRGFVSGIIT 187

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OY 186 IYRAAYFGIYDTAKGMLPDPKNTIHIVISMMIAQTVTAAGLTSYFPDVTVRMMQSGRK 245
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 188 IYRAAYGFPDTRAGMLPDKRNTPIYISMAIAQVTVTAAGIVSTFPDVTVRMMQSGRK 247
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 246 GTDIMYTGTLDCWKRIARDEGKAFFGAGSNVLRGSGAFVLVLYDEIKKY 297
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 248 ATEIITYKNTLHCWNTIAKQGTGAFKGFAGFSNVLRGTGAGAFVLVLYDEIKKF 299

RESULT 9
OY 044093 PRELIMINARY; PRT; 288 AA.
ID 044093:
AC 044093:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE ADP/ATP TRANSLUCASE (FRAGMENT).
GN SESB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Cameron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL: AF025798; AAB87883.1; -.
DR FlyBase: FBgn0023292; Dpse\sesb.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.
KM Inner membrane: Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1190.5; DB 5; Length 288;
Best Local Similarity 80.4%; Pred. No. 9.4e-99;
Matches 228; Conservative 20; Mismatches 33; Indels 3; Gaps 3;
OY 5 ALSFAKDFLAGVAAAIKTAAPARIEKVKLLQVQHASKOITADKQYKGIIDCVIRIPE 64
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 7 AIGFVKDFAGGISAASVSKTAVAPIERVKLLQVQHISKQISPDQKQYKGMVDCFLRIPE 66
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 65 QEVLSFMRGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKRTQFWRFFAGNLASGGAAG 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 67 QGFSSFWRGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKNTQFWRFFAGNLASGGAAG 126
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 125 ATSLCFVYPLDFARTRLAADVGKAGAEERFRLGDLCKVIKYSKQIKGLYGFNVSVGI 184
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 127 ATSLCFVYPLDFARTRLAADVGK-GGQREFGLGNCILKIFKSGDLVGLYGFVSVGI 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 185 IYRAAYFGIYDTAKGMLPDKRNTIHIVISMMIAQTVTAAGLTSYFPDVTVRMMQSGR 244
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 186 IYRAAYFGIYDTAKGMLPDKRNTIHIVISMMIAQTVTAAGLTSYFPDVTVRMMQSGR 244
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 245 KGTDIMYTGTLDCWKRIARDEGKAFFGAGSNVLRGSGAFVLV 289
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 245 KATEIITYKNTLHCWNTIAKQE-GSAFFKGFAGFSNVLRGTGAGAFVLV 288

RESULT 10
OY 044094 PRELIMINARY; PRT; 288 AA.
ID 044094:
AC 044094:
DT 01-JUN-1998 (TREMBLrel. 06, Created)

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DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLUCASE (FRAGMENT).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Cameron J.M., Chen B., Kreitman M.;
RL Genetica 0:0-0(1997).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
EMBL: AF025799; AAB87884.1; -.
DR FlyBase: FBgn0023237; Dsub\sesb.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carrier.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER.
KM Inner membrane: Mitochondrion; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.6%; Score 1185.5; DB 5; Length 288;
Best Local Similarity 80.0%; Pred. No. 2.6e-98;
Matches 228; Conservative 21; Mismatches 33; Indels 3; Gaps 3;
OY 5 ALSFAKDFLAGVAAAIKTAAPARIEKVKLLQVQHASKOITADKQYKGIIDCVIRIPE 64
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 7 AMGFVKDFAGGISAASVSKTAVAPIERVKLLQVQHISKQISPDQKQYKGMVDCFLRIPE 66
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 65 QEVLSFMRGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKRTQFWRFFAGNLASGGAAG 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 67 QGFSSFWRGNLANIYRFPPTQALNFAFKDKYKQIFLGVDKNTQFWRFFAGNLASGGAAG 126
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 125 ATSLCFVYPLDFARTRLAADVGKAGAEERFRLGDLCKVIKYSKQIKGLYGFNVSVGI 184
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 127 ATSLCFVYPLDFARTRLAADVGK-GGQREFGLGNCILKIFKSGDLVGLYGFVSVGI 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 185 IYRAAYFGIYDTAKGMLPDKRNTIHIVISMMIAQTVTAAGLTSYFPDVTVRMMQSGR 244
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 186 IYRAAYFGIYDTAKGMLPDKRNTIHIVISMMIAQCVTVTAAGIVSTFPDVTVRMMQSGR 244
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 245 KGTDIMYTGTLDCWKRIARDEGKAFFGAGSNVLRGSGAFVLV 289
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 245 KATEIITYKNTLHCWNTIAKQE-GTAFKGFAGFSNVLRGTGAGAFVLV 288

RESULT 11
OY 025129 PRELIMINARY; PRT; 304 AA.
ID 025129:
AC 025129:
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLUCASE.
GN HRATL.
OS Haemaphysalis foveolatus (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Haemaphysalis.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE FROM N.A.
RA Miya T.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.
RA Miya T., Makabe K., Satoh N.;

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RA Thierly-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Steilyes L.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL; 080931; AAB38001.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mlt_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;

Query Match 66.5%; Score 1029; DB 5; Length 313;
 Best Local Similarity 70.8%; Pred No. 3.2e-84;

Matches 206; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

OY 8 FAKDELAGVAAAIKSTAVAPIERVKLLDQVHASKQITADKQKGIIDCVVRIPKEQEV 67
 DB 25 FLIDLASGCTAAASKTAVAPIERVKLLDQVHASKQITADKRYKGIIDVLRVPREQGY 84
 OY 68 LSFWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFWRYPAGNLASGAAGATS 127
 DB 85 AALWRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFWRYPAGNLASGAAGATS 144
 OY 128 LCFVYPLDFARTRLADAVGKAGAREFRGLDGLVRYKSDGIKGLYOGFNVSVOGIITY 187
 DB 145 LCFVYPLDFARTRLADAVGKAN-EREFKGLADCLVIAKSDGPIGLYRGFFVSVOGIITY 203
 OY 188 RAAVFGIYDTAKGML-PDEKNTNIVISWMIQOTVAVAGLTSYPEDTVRRMMQSGRKG 246
 DB 204 RAAVFGMEPTAKMFTADGKLNFFAAMAIAQVTVGSGILSYPMDTVRRMMQSGRK- 262
 OY 247 TDIMYTGTLDCGKRLIARDGSKAFKFGAMSNTLRMGCAFVLVIYDEIKKY 297
 DB 263 -DVLKNTLDCAVKIKKEGMSAMFEGALSNVFRGTGGALVLAIDELQKF 312

Search completed: February 13, 2002, 09:34:15
 Job time: 172 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:34:42 ; Search time 22.53 Seconds

(Without alignments)
484.959 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDALSPFAKDFLAGVAA.....LRMGAFVLVLYDEIKKKT 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SWISSPROT_39.*

Listing first 45 summaries

Result No. Score Match Length DB ID

1 1537 99.4 298 1 ADT2_HUMAN

2 1525 98.6 298 1 ADT2_HUMAN

3 1519 98.2 298 1 ADT2_MOUSE

4 1458 94.2 298 1 ADT3_BOVIN

5 1454 94.0 298 1 ADT3_HUMAN

6 1417 91.6 298 1 ADT1_RAT

7 1414 91.4 297 1 ADT1_BOVIN

8 1413 91.3 298 1 ADT1_HUMAN

9 1411 91.2 298 1 ADT1_MOUSE

10 1218.5 78.8 301 1 ADT_DROME

11 1190 76.9 301 1 ADT_ANOXA

12 968 62.6 339 1 ADT_CHLKE

13 771 49.8 386 1 ADT_GOSHI

14 770 49.8 322 1 ADT_SCHPO

15 765 49.5 307 1 ADT_CHLRE

16 761.5 49.2 387 1 ADT3_YEAST

17 759 49.1 387 1 ADT1_MAIZE

18 757 48.9 313 1 ADT1_NEUCR

19 753 48.7 387 1 ADT1_MAIZE

20 752.5 48.6 318 1 ADT2_YEAST

21 752 48.6 386 1 ADT1_SOLITU

22 750 48.5 382 1 ADT_ORYSA

23 749.5 48.4 305 1 ADT_KITUA

24 747.5 48.3 381 1 ADT1_ARATH

25 745.5 48.2 385 1 ADT1_ARATH

26 744 48.1 331 1 ADT2_SOLITU

27 741.5 47.9 336 1 ADT2_WHEAT

28 737 47.6 331 1 ADT1_WHEAT

29 728 47.1 309 1 ADT1_YEAST

30 707 19.8 587 1 CMG3_CAEBL

31 302 19.5 587 1 CMG3_CAEBL

32 285 18.4 350 1 GDC_BOVIN

33 284 18.4 307 1 YOTL_YEAST

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description

P05141 Homo sapien
Q09073 Rattus norv
P11881 Mus musculu
P12007 Bos taurus
P12236 Homo sapien
Q05962 Rattus norv
P02722 Bos taurus
P12235 Homo sapien
P18962 Homo sapien
Q26365 Drosophila
Q27238 Anopheles g
P11692 Chlorella x
O02342 Gossypium h
Q09188 Schizosacch
P27080 Chlamydomon
P18238 Saccharomyc
P04709 Zea mays (m
P02723 Neurospora
P12857 Zea mays (m
P18239 Saccharomyc
P25083 Solanum tub
P11691 Oryza sativ
P49382 Kluyveromyc
P1167 Arabidopsis
Q10941 Arabidopsis
P41629 Trifolium ae
P27081 Solanum tub
Q1630 Trifolium ae
P04710 Saccharomyc
Q26799 Saccharomyc
Q15329 Caenorhabdi
Q01888 Bos taurus
Q09297 Saccharomyc

ALIGNMENTS

34 278 18.0 322 1 BMC2_MOUSE
35 276.5 17.9 322 1 GDC_RAT
36 276.5 17.9 702 1 CMG1_CAEBL
37 276 17.8 678 1 BMC2_HUMAN
38 274 17.7 325 1 BMC2_HUMAN
39 265.5 17.2 332 1 GDC_HUMAN
40 261.5 16.9 675 1 BMC2_HUMAN
41 249.5 16.1 326 1 YER08_SCHPO
42 249 16.1 324 1 PRT_YEAST
43 249 16.1 676 1 CMG2_MOUSE
44 249 16.1 695 1 CMG1_DROME
45 247 16.0 312 1 UCP3_HUMAN

RESULT 1
ADT2_HUMAN
ID ADT2_HUMAN STANDARD: PRT: 298 AA.
AC P05141: Q43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP-ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
GN SLT25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
cloning and sequence."
RT J. Biol. Chem. 265:16060-16063(1990).
[2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
growth-regulated."
RT J. Biol. Chem. 262:4355-4358(1987).
[3]
RN RP SEQUENCE FROM N.A.
RA Chen C.-N., Su Y., Baybayan P., Siruno A., Nagaraja R.,
Mazarella R.A., Schlesinger D., Chen E.Y.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
[4]
RN RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozersky P.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[5]
RN RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver."
RT Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
[6]
RN RP FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
MITOCHONDRIAL INNER MEMBRANE.
[7]
RN RP SUBUNIT: HOMODIMER.
[8]
RN RP SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
INNER MEMBRANE.
[9]
RN RP DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
[10]
RN RP SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
[11]
RN RP THIS SWISS-PROT entry is copyright. It is produced through a collaboration

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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC EMBL: M57424; AAA51737.1; -
 DR EMBL: J02683; AAA35579.1; -
 DR EMBL: J78810; AAB39266.1; -
 DR EMBL: AC004000; AAB96347.1; -
 DR EMBL: J03591; AAA36749.1; -
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR MIM: 300150; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3-
 DR PRINTS: PR00927; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KN Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).
 FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 99.4%; Score 1537; DB 1; Length 298;
 Best Local Similarity 99.3%; Pred. No. 9.5e-130;
 Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDALSFADKPLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 QY 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGKLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGKLYOGFNVS 180
 QY 181 VGGIIYRAAYFGIYDTAGMLPDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 DB 181 VGGIIYRAAYFGIYDTAGMLPDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 QY 241 QSGRKGTDMYTGTLDCMKRIADDEGKAFKFGAMSNVLRGMGAFVLYLYDEIKKYYT 298
 DB 241 QSGRKGTDMYTGTLDCMKRIADDEGKAFKFGAMSNVLRGMGAFVLYLYDEIKKYYT 298

RESULT 2
 ADP2_RAT
 ID ADP2_RAT STANDARD: PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADP, ATP CARRIER PROTEIN, FLIBROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
 DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).

GN SLG25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinozuka Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RL encoding rat mitochondrial adenine nucleotide translocator";
 RT Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC -1- MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 CC INNER MEMBRANE.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE MITOCHONDRIAL CARRIER FAMILY.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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 or send an email to license@isb-sib.ch).

CC EMBL: D12771; BAA02238.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00927; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KN Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EFE35 CRC64;

Query Match 98.6%; Score 1525; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 1.1e-128;
 Matches 293; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTDALSFADKPLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYKGIIDCVVR 60
 QY 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEQVLSFWNGNLNVIRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGKLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFRGLGDLVYIKYSDGIGKLYOGFNVS 180
 QY 181 VGGIIYRAAYFGIYDTAGMLPDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 DB 181 VGGIIYRAAYFGIYDTAGMLPDPKNTHTIVISWMTAQVTAVAGLTSYPTDVRRRMM 240
 QY 241 QSGRKGTDMYTGTLDCMKRIADDEGKAFKFGAMSNVLRGMGAFVLYLYDEIKKYYT 298

Db 241 QSGRKGTDIWVTGLDQWRKIARDEGKAFFKGAMSNVLRMGAFVLYLYDEIKKYY 298

RESULT	3
ADT2_MOUSE	

DT 01-OCT-1996 (Rel. 34, created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 20-AUG-2001 (Rel. 40, last annotation update)
DE ADP-ATP CARRIER PROTEIN, FIROBLAST ISOFORM (ADP/ATP TRANSLOCASE 2)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 2) (ANT 2).
GN SLK25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SRRAIN-C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RT Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
homologs."; *Nat. Genet.* 7:25-30(1996).

DR	EMBL: U27516:	AAC52838.1;	-
DR	EMBL: U10404:	AAAI9009.1;	-
DR	EMBL: X70847:	CAA50196.1;	-
DR	MGI: 1353496:	Slc25a5.	
DR	InterPro: IPR002067:	Mit_carrier.	
DR	InterPro: IPR001993:	Mitoch_carrier.	
DR	Pfam: PF00153:	mito_carr; 3.	
DR	PRINTS: PR00926:	MITOCARRIER.	
DR	PRINTS: PR00927:	ADPTRNSLASE.	
DR	PROSITE: PS00215:	MITOCH_CARRIER; 3.	
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;		
KW	Multigene family.		
KW	TRANSMEM	12	29
FT	TRANSMEM	73	91
FT	TRANSMEM	117	134
FT	TRANSMEM	176	195
FT	TRANSMEM	214	231

FT	TRANSMEM	273	291	6 (POTENTIAL).
FT	REPEAT	1	111	1.
FT	REPEAT	112	208	2.
FT	REPEAT	209	298	3.
SO	SEQUENCE	298 AA;	32931 MM;	0798E04B987EEF20 CRC64;

Qy	1	MTDAALSFANKEFLAGGVAALAAISTKAAVPIEBVKLLLOVHAASKITADKQYKGIIDCVR	60
Db	1	MTDAAVSFANKEFLAGGVAALAAISTKAAVPIEBVKLLLOVHAASKITADKQYKGIIDCVR	60
Qy	61	IPKEOEVLSEWNGMLANVIRYPTQALNFAKDKYKOIFLGVDKRTQEMRYFAGNLASG	120
Db	61	IPKEOGVLSFWRGNMLANVIRYPTQALNFAFKDKYKOIFLGVDKRPQFWRFYFAGNLASG	120
Qy	121	GAACATSLCFEYPLDPFARTRLAAAVGKAGAEERERKGGDCLVYIKSDGIRKGLQGNVS	180
Db	121	GAACATSLCFEYPLDPFARTRLAAAVGKAGAEERERKGGDCLVYIKSDGIRKGLQGNVS	180
Qy	181	VQGIIVYRAAFYGLIDPAKAGMLDPDKMTHIYISMIQOTYTAAGLTSYEPDQYVRRMM	240
Db	181	VQGIIVYRAAFYGLIDPAKAGMLDPDKMTHIYISMIQSVTAAGLTSYEPDQYVRRMM	240
Qy	241	QSGKRGDIDMTGTLDDCMRKARBEQSGKAPFKGMSVNLGMSGAFVLVLYDELKATY	298
Db	241	QSGKRGDIDMTGTLDDCMRKARBEQSGKAPFKGMSVNLGMSGAFVLVLYDELKATY	298

RESULT	4			
ADT3_BOVIN		STANDARD:	PRF:	298 AA.
ID	ADT3_BOVIN			
AC	P32007;			
DT	01-JUL-1993 (Rel. 26, Created)			
DT	01-JUL-1993 (Rel. 26, Last sequence update)			
DT	20-JUG-2001 (Rel. 40, Last annotation update)			
DE	ADP/ATP CARRIER PROTEIN, ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).			
DE	NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).			
GN	SLC25A6 OR ANT3.			
OS	Bos taurus (bovine).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89229093; PubMed=2540808;			
RA	Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;			
RT	"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";			
RL	Biochemistry 28:866-873(1989).			
CC	-1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.			
CC	-1 SUBUNIT: HOMODIMER.			
CC	-1 SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE.			
CC	-1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
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CC	or send an email to license@sib-sb.ch).			
DR	EMBL; M24103; AAA30769.1; -			
DR	PIR; B43646; B43646.			
DR	InterPro; IPR002067; Mit_carrier.			

DR EMBL; M24103; AAA30769.1; - .
DR PIR; B43646; B43646.
DR InterPro; IPR002067; Mlt_carrier

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DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carrier.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
   Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match
Best Local Similarity 94.2%; Score 1458; DB 1: Length 298;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLLOVGHASKQITADKQYKGIIDCVVR 60
DB 1 MTEQAISFAKDFLAGGIAAIAIKSTAVAPIERVKLLLOVGHASKQIADKQYKGIIDCVVR 60
QY 61 IPREQEVLSEFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
DB 61 IPREQEVLSEFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAKRTLADVKGAGAREFRGIGDCLVYIYKSDGIGKLYCGFNVS 180
DB 121 GAAGATSLCFVYPLDPAKRTLADVKGAGAREFRGIGDCLVYIYKSDGIGKLYCGFNVS 180
QY 181 VOGIIYRAAYFGIYDTAKMLDPKNTHTIVISMIAQOTTAAGLTSYEPDTPVRRMM 240
DB 181 VOGIIYRAAYFGIYDTAKMLDPKNTHTIVISMIAQOTTAAGLTSYEPDTPVRRMM 240
QY 241 QSGRKGTIDMYTGLDCKRKIARDEGKAFFKGAMSVNLKMGAFVLYLDEIKK 296
DB 241 QSGRKGDIMYTGTVDCWKRIKDEGKAFFKGAMSVNLKMGAFVLYLDEIKK 296

RESULT 5
ADP3_HUMAN
ID ADP3_HUMAN STANDARD: PRT; 298 AA.
AC P12236;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3)
DE (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3).
GN SLG25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RP [2]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).

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CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J03592; AAA36750.1; -.
DR PIR: S03894; S03894.
DR PIR: B28116; B28116.
DR MIM: 300151; -.
DR MIM: 403000; -.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carrier.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
   Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 2).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;

Query Match
Best Local Similarity 94.0%; Score 1454; DB 1: Length 298;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLLOVGHASKQITADKQYKGIIDCVVR 60
DB 1 MTEQAISFAKDFLAGGIAAIAIKSTAVAPIERVKLLLOVGHASKQIADKQYKGIIDCVVR 60
QY 61 IPREQEVLSEFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
DB 61 IPREQEVLSEFWRGNLAVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAKRTLADVKGAGAREFRGIGDCLVYIYKSDGIGKLYCGFNVS 180
DB 121 GAAGATSLCFVYPLDPAKRTLADVKGAGAREFRGIGDCLVYIYKSDGIGKLYCGFNVS 180
QY 181 VOGIIYRAAYFGIYDTAKMLDPKNTHTIVISMIAQOTTAAGLTSYEPDTPVRRMM 240
DB 181 VOGIIYRAAYFGIYDTAKMLDPKNTHTIVISMIAQOTTAAGLTSYEPDTPVRRMM 240
QY 241 QSGRKGTIDMYTGLDCKRKIARDEGKAFFKGAMSVNLKMGAFVLYLDEIKK 296
DB 241 QSGRKGDIMYTGTVDCWKRIKDEGKAFFKGAMSVNLKMGAFVLYLDEIKK 296

RESULT 6
ADP1_RAT
ID ADP1_RAT STANDARD: PRT; 298 AA.
AC Q05962;
DT 01-FEB-1994 (Rel. 28, Last sequence update)

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20-AUG-2001 (Rel. 40, last annotation update)
 ADP-ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
 TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
 GN SLIC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=SPRAGUE-DAWLEY, AND WISTAR; TISSUE=Heart, and Liver;
 RA MEDLINE=94002161; PubMed=8399300;
 RX Shiohara Y., Kamida M., Yamazaki N., Terada H.;
 RT Isolation and characterization of cDNA clones and a genomic clone
 encoding rat mitochondrial adenine nucleotide translocator.;
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 INNER MEMBRANE.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X61667; CAA3842.1; -
 DR EMBL: D12770; BAA0237.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; MitoCh_carrier.
 DR Pfam: PF00153; mito_carr; 3
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32989 MW; 66704EF78C6BC320 CRC64;
 Query Match 91.6%; Score 1417; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 4.6e-119;
 Matches 266; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

|||||
 DB 181 VGGIIIRAAVFGIYDPAKMLDPKNTHTIVISWMIQOTVAVAGLTSYFPDVRRRMM 240
 OY 241 QSRKRGTDIWTGTLDCKRKRIARDEGKAFFKGAWSNVLRGKGAFVLYDEIKRY 297
 DB 241 QSRKRGADIWGTGTCVCKRKRIARDEGKAFFKGAWSNVLRGKGAFVLYDEIKRY 297
 RESULT 7
 ID ADT1_BOVIN STANDARD; PRT; 297 AA.
 AC P02722;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ADP-ATP CARRIER PROTEIN, HEART ISOFORM T1 (ADP/ATP TRANSLOCASE 1)
 DE (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
 GN SLIC25A4 OR ANT1.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP MEDLINE=89229093; PubMed=2540808;
 RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
 RT Two bovine genes for mitochondrial ADP/ATP translocase expressed
 differences in various tissues.;
 RL Biochemistry 28:866-873(1989).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=82188267; PubMed=7076130;
 RA Aquila H., Mista D., Eulitz M., Klingenberg M.;
 RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
 mitochondria.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
 RN [3]
 RP SEQUENCE OF 207-297 FROM N.A.
 RX MEDLINE=86293775; PubMed=3017341;
 RA Rasmussen U.B., Wohlrab H.;
 RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
 an unusually short 3'-noncoding sequence.";
 RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
 INNER MEMBRANE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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 CC
 CC EMBL: M13783; AAA30363.1; -
 DR EMBL: M24102; AAA30768.1; -
 DR PIR: A03181; XWBO
 DR PIR: A24822; A24822.
 DR PIR: A43646; A43646.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR001993; MitoCh_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00927; ADPTRNSLCASE.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Methylation.

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FT INIT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AEB48 CRC64;

Query Match 91.4%; Score 1414; DB 1; Length 297;
Best Local Similarity 89.9%; Pred. No. 8,6e-119;
Matches 265; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 2 TDAALSFADPLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRI 61
DB 1 SQAALSLFLKDLGAVAAAIKSTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRI 60
QY 62 PREQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 121
DB 61 PREQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 122 AAGATSLCFVPLDFAPRLADVGKAGAREPFGDCLVITYKSDGIKGLYOGFNVS 181
DB 121 AAGATSLCFVPLDFAPRLADVGKAGAREPFGDCLVITYKSDGIKGLYOGFNVS 180
QY 182 OGIIIRAAVEGIYDTAKGMLDPKNTALIVSMIAQVTAVALGSLTSPEDTVRRMMQ 241
DB 181 OGIIIRAAVEGIYDTAKGMLDPKNTALIVSMIAQVTAVALGSLTSPEDTVRRMMQ 240
QY 242 SRRKGTDMYTTGLDCKRIADDEGKAFKFGKANSVNLGMCAGAYLVLYDEIKY 297
DB 241 SRRKGTDMYTTGLDCKRIADDEGKAFKFGKANSVNLGMCAGAYLVLYDEIKY 296

RESULT 8
ADFL_HUMAN STANDARD; PRT; 298 AA.
AC P12235;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP-ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li K., Warner C.K., Hodges J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT is located on chromosome 4, and is differentially expressed."
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;

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RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and convolution with mitochondrial DNA genes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE OF 1-37 FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -I- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -I- SUBUNIT: HOMODIMER.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC INNER MEMBRANE.
CC -I- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -I- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: J02966; AA61233.1; -
DR EMBL: J03593; AA636751.1; -
DR EMBL: J04982; AA51736.1; -
DR PIR: A28116; A28116.
DR PIR: A39891; A39891.
DR PIR: S03893; S03893.
DR PIR: A44778; A44778.
DR MIM: 103220;
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 16 16 G -> A (IN REF. 3).
FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
FT CONFLICT 227 227 V -> L (IN REF. 3).
SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAEC4E7CFBB CRC64;

Query Match 91.3%; Score 1413; DB 1; Length 298;
Best Local Similarity 89.2%; Pred. No. 1.1e-118;
Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSFADPLAGVAAAIKSTAVAPIERVKLLQVQHASKQITADKQYGIIDCVRI 60
DB 1 MTDHMSFLKDLGAVAAAIKSTAVAPIERVKLLQVQHASKQISAEKQYGIIDCVRI 60
QY 61 IPKEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
DB 61 IPKEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
QY 121 GAAGATSLCFVPLDFAPRLADVGKAGAREPFGDCLVITYKSDGIKGLYOGFNVS 180

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Db 121 GAAGATSLCFVYPLDPAFRLADVKGAAQREFHGLDCTIIKIFKSDGLRGHYGFFNVS 180
QY 181 VGGITIRAAVFGIYDPAKMLDPKKNTHIVISMIAQOTAVAGLTSYFEDVRRRMM 240
Db 181 VGGITIRAAVFGIYDPAKMLDPKKNTHIVISMIAQOTAVAGLTSYFEDVRRRMM 240
QY 241 QSRKGTIDIMYTGTLDCKMRKIADEGKAFKFGAMSVNLGKMGAFVLVYDEIRKY 297
Db 241 QSRKGTIDIMYTGTLDCKMRKIADEGKAFKFGAMSVNLGKMGAFVLVYDEIRKY 297

RESULT 9
ADP1_MOUSE STANDARD: PRT: 298 AA.
AC P48962;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP
DE TRANSLOCASE 1) (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. Genome 7:25-30(1996).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN; MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC -----
DR EMBL: U27315; AAC52837.1; -
DR MGD: MGI:1353495; SLC25a4.
DR InterPro: IPR002067; MitCarrier.
DR InterPro: IPR001993; MitochCarrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29
FT TRANSMEM 73 91
FT TRANSMEM 117 134
FT TRANSMEM 176 195
FT TRANSMEM 214 231
FT TRANSMEM 273 291
FT REPEAT 1 110
FT REPEAT 111 208
FT REPEAT 209 298
FT REPEAT 209 298
SQ SEQUENCE 298 AA; 32870 MW; 32AC3B4EFCFA482 CRC64;

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Query Match 91.2%; Score 1411; DB 1; Length 298;
Best Local Similarity 89.2%; Pred. No. 1,6e-118;

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Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
QY 1 MTPAALSFADPLAGVAAAIISKTAAPERVRKLLLOVGHASKOIRADKQKIIICVVR 60
Db 1 MGDALSLFDPLAGIAAASVTAAPIERVRLKLLLOVGHASKOISAEKQKIIDCVVR 60
QY 61 IPKEQELVSWRGNLNVIRYPTQALNFAFKDKYKOIFEGYDKRQTFQFRYFAGNLASG 120
Db 61 IPKEQGLSWRGNLNVIRYPTQALNFAFKDKYKOIFEGYDKRQTFQFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDPAFRLADVKGAAQREFHGLDCTIIKIFKSDGLRGHYGFFNVS 180
Db 121 GAAGATSLCFVYPLDPAFRLADVKGAAQREFHGLDCTIIKIFKSDGLRGHYGFFNVS 180
QY 181 VGGITIRAAVFGIYDPAKMLDPKKNTHIVISMIAQOTAVAGLTSYFEDVRRRMM 240
Db 181 VGGITIRAAVFGIYDPAKMLDPKKNTHIVISMIAQOTAVAGLTSYFEDVRRRMM 240
QY 241 QSRKGTIDIMYTGTLDCKMRKIADEGKAFKFGAMSVNLGKMGAFVLVYDEIRKY 297
Db 241 QSRKGTIDIMYTGTLDCKMRKIADEGKAFKFGAMSVNLGKMGAFVLVYDEIRKY 297

RESULT 10
ADT_DROME STANDARD: PRT: 297 AA.
AC Q26365; Q26254; P91614; Q9V270;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ADP/ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
DE TRANSLOCATOR) (ANT) (STRESS SENSITIVE B PROTEIN).
GN SESB OR A/A-T OR CG16944.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92389367; PubMed=1387687;
RA Louvi A., Tsililou S.G.;
RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
RT melanogaster shows a high degree of similarity with the mammalian
RT ADP/ATP translocases."
RL J. Mol. Evol. 35:44-50(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=94350065; PubMed=7520869;
RA Hutter P., Karch F.;
RT "Molecular analysis of a candidate gene for the reproductive
RT isolation between sibling species of Drosophila."
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN=OREGON-R;
RA Zhang Y.O., Davis A.W., Roote J., Herrmann S., Ashburner M.;
RA Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wen K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandal D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA Cherry J.M., Dawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablo S., Gaudelocher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibeagwu C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei V., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J.J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacleby J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinelt K., Remington K., Saunders R.D.C., Schaefer F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syvras K.R., Tector C., Turner R., Venter E., Weiss A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Wengenbach J.,
RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: S43651; AAB23114.1; -;
DR EMBL: S71762; AAB31734.3; -;
DR EMBL: Y10618; CAA71628.1; -;
DR EMBL: AE003464; AAF47957.1; -;
DR FlyBase; FBgn0003360; sepb.
DR InterPro; IPR002067; mt_carrler.
DR InterPro; IPR001993; mtloch_carrler.
DR Pfam; PF00153; mtlo_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER.
DR PROSITE; PS00927; ADPTRNSLASE.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
KW Transmem 14 31 1(POTENTIAL).
FT TRANSMEM 75 93 2(POTENTIAL).
FT TRANSMEM 119 136 3(POTENTIAL).
FT TRANSMEM 177 196 4(POTENTIAL).
FT TRANSMEM 214 231 5(POTENTIAL).
FT TRANSMEM 272 290 6(POTENTIAL).
FT CONFLICT 18 19 QV -> GI (IN REF. 3 AND 4).
FT CONFLICT 81 81 I -> Y (IN REF. 1).
FT CONFLICT 200 200 R -> RG (IN REF. 3 AND 4).
FT CONFLICT 266 266 C -> A (IN REF. 2).
FT CONFLICT 267 268 PC -> TGA (IN REF. 3 AND 4).
FT CONFLICT 268 268 C -> S (IN REF. 1).
SQ SEQUENCE 237 AA: 32880 MW: 35943.9568 EF9750 CRC64.

Query Match	78.8%	Score 1218.5	DB 1	Length 297
Best Local Similarity	80.5%	Pred. No. 2.2e-101		
Matches 235	Conservative 20	Mismatches 34	Indels 3	Gaps 3

Oy	5	ALSKAPQELAGVAAALSTKTAVALPERKLLLYOVHASKOTADQYGGIIDDVCVRIRKE	64
Dd	7	AVGEVKDFEAAQOVAASAKTIVAPERKLLLYOVHISKOLSPDQIKGMWDCFRIRKE	66
Oy	65	QEVLSFWMGNIANVIKREPTQALNFAFKDKYKOJFLGVDVRTQFWRYPAGNLASGAAG	124
Dd	67	QGFSSEMRGNLANVIKRPPTQALNFAPFDKKYQVPLGVDRNTQGWRYEAGNLASGAAG	126
Oy	125	ATSLCFVPPLDPARTRLAADYGKAGEEFGLGDCLVKIYKSDBGIKGLYGFNVSVOGI	184
Dd	127	ATSLCFVPLDPFARTRLAADYTK--GGQREFPGLGNCILKIRKSDSIVOLYGFVSVOGI	185
Oy	185	IIVRAAYGVIDFTAKGMLPDPRKNHFIVISMMIAQVTVTAGITSPFPYVRRMMOSGR	244
Dd	186	IIVRAAYGFEPDTAR-MLPDRKNPTFIYSMAIAQVTVTAGIVSTPFTVRRMMOSGR	244
Oy	245	KGTIDIMYTGLTDWCWKRIARDEGKAFFKGAAASNVLRGSGAFVLYLDEIKR	296
Dd	245	KATEIYKNTLHCWATIAKQE-GPCFFFGARSNILRGIGAFVLYLDEIKR	295
<hr/>			
RESULT 11			
ID	ADT_ANOGA	STANDARD:	PRT: 301 AA.
AC	Q27238		
DT	01-NOV-1997	(Rel. 35, Created)	
DT	01-NOV-1997	(Rel. 35, Last sequence update)	
DT	01-NOV-1997	(Rel. 35, Last annotation update)	
DE	ADP, ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE		
DE	TRANSLOCATOR) (ANT).		
OS	Anopheles gambiae (African malaria mosquito).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;		
OX	Anopheles.		
RX	NCBI_Taxid:7165:		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=G3;		
RX	MEDLINE=94348635; PubMed=8069414;		
RA	Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.;		
RT	"A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles		
RT	gambiae.";		
RL	Insect Mol. Biol. 3:35-40(1994).		
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE		
CC	MITOCHONDRIAL INNER MEMBRANE.		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL		
CC	INNER MEMBRANE.		
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.		
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.		
CC	-----		
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CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL, L11618; AAB04104.1; -;		
DR	EMBL, L11617; AAB04105.1; -;		
DR	InterPro: IPR002067; Mit_carrier.		
DR	InterPro: IPR001993; Mitoch_carrier.		
DR	Pfam: PF00153; mito_carr; 3.		
DR	PRINTS: PR00926; MITOCARRIER.		
DR	PRINTS: PR00927; ADPTRNSLCASE.		
DR	PROSITE, PS00215; MITOCH_CARRIER, 3.		
FM	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.		
FT	TRANSMEM 14 31 1(POTENTIAL).		
FT	TRANSMEM 75 93 2(POTENTIAL).		
FT	TRANSMEM 119 136 3(POTENTIAL).		
FT	TRANSMEM 178 197 4(POTENTIAL).		


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DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transit peptide; Multigene family.
FT TRANSIT 1 76 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 77 386 ADP/ATP CARRIER PROTEIN 1.
FT TRANSMEM 90 107 1 (POTENTIAL).
FT TRANSMEM 152 170 2 (POTENTIAL).
FT TRANSMEM 195 212 3 (POTENTIAL).
FT TRANSMEM 256 275 4 (POTENTIAL).
FT TRANSMEM 295 312 5 (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
SQ SEQUENCE 386 AA; 42093 MW; A05F76C73FECDEE6 CRC64;

Query Match          49.8%; Score 771; DB 1; Length 386;
Best Local Similarity 55.4%; Pred. No. 2.2e-61;
Matches 169; Conservative 35; Mismatches 79; Indels 22; Gaps 7;

OY 7 SFAPDLGAGVAAAIKSTAVAPIERVKLLQVO-HASKQITADKQGIIDCVIRIPKEQ 65
DP 85 SFADIDLMGVSAAVSKTAAPIERVKLLIQNDDEMIKSGRLSEPKYKGIIDCFKRTIKDE 144
OY 66 EVLSFMRGLANVIRFPPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 125
DB 145 GEGSLMRGNTANVIRFPPQALNFAFKDKYKRLFNFKKD-RDGYKWFAGNLASGAGA 203
OY 126 TSLSFVYPLDPFARTRLAAD-VGKAGAREFRGLGDCLVKITYKSDGIKGYGFENVYOG 183
DB 204 SSSLFVYSLDYARTRLANDAKAKKGGEROFNGLVYRKRTLSKDSITAGLRKFNISCVG 263
OY 184 IIRAYRFGIYDTAK-----GMLPDPKNTNIVISMIAQVTAVAGLTSYPTDVRRRM 238
DB 264 IIVRYRLYFGMVDLSKPVLLTSGMQDSFFASFYLGWLI-----TNGAALASYPIDTVRRRM 319
OY 239 MMSGKRGKIDIMTGTLDCKRKIARDEGKAFPKGAMSVNLKMGAFVLYLVDL----- 294
DB 320 MMTSGKA---VKYKSSLDLAFSOLTKNEGKSLFKGAGSNILRAIAGVLAGYDKLQILIV 376
OY 295 --KKY 297
DB 377 FGKKY 381

RESULT 14
ADT_SCHPO
ID ADT_SCHPO STANDARD: PRT: 322 AA.
AC 009188;
DT 01-NOV-1997 (rel. 35, Created)
DT 01-NOV-1997 (rel. 35, Last sequence update)
DT 15-DEC-1998 (rel. 37, Last annotation update)
DE ADP/ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
DE TRANSLOCATOR) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA MEDLINE=96257204; PubMed=8675018;
RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
RT "Cloning of the gene encoding the mitochondrial adenine nucleotide
RT carrier of Schizosaccharomyces pombe by functional complementation in
RT Saccharomyces cerevisiae.";
RL Gene 171:113-117(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Lyne M., Wood V., Rajandream M.A., Barrell B.G., Rieger M.;

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RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC -----
DR EMBL: Z49974; CA90275.1; -
DR EMBL: AL023634; CNA19176.1; -.
DR HSP: P04002; IATF.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00927; ADPTRNSLCASE.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 28 48 1 (POTENTIAL).
FT TRANSMEM 93 111 2 (POTENTIAL).
FT TRANSMEM 131 151 3 (POTENTIAL).
FT TRANSMEM 197 217 4 (POTENTIAL).
FT TRANSMEM 222 242 5 (POTENTIAL).
FT TRANSMEM 289 309 6 (POTENTIAL).
SQ SEQUENCE 322 AA; 35020 MW; 8AC3D16A40F41AFC CRC64;

Query Match          49.8%; Score 770; DB 1; Length 322;
Best Local Similarity 53.6%; Pred. No. 2.2e-61;
Matches 158; Conservative 51; Mismatches 74; Indels 12; Gaps 6;

OY 7 SFAPDLGAGVAAAIKSTAVAPIERVKLLQVOHASKQITADK---OYKGIIDCVIRIPK 63
DB 26 TFFDFPMGVSAAVSKTAAPIERVKLLIQND--DEMIRARGLSHRKIGICECKRTAA 83
OY 64 EGVLSFMRGLANVIRFPPQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASGAA 123
DB 84 EGVLSLMRGNTANVIRFPPQALNFAFKDKKMF-GYKKERDGYAKWFAFNLASGAA 142
OY 124 GATSLCFVYPLDPFARTRLADY--GKAGAREFRGLGDCLVKITYSDGIKGYGFENVY 181
DB 143 GAASLFFVYSLDYARTRLANDAKSAKKGGEROFNGLVYRKRTYRSDGLRGYRGFSPV 202
OY 182 OGIIIRAYRFGIYDTAKG-MLPDPKNTNIVISMIAQVTAVAGLTSYPTDVRRRM 240
DB 203 VGIIYRGLYFGKIDTLKRVVLVGLPGLNPLASFLIGAVNTGSGVASYPLDTIRRRM 262
OY 241 OSGRKQIDIMTGTLDCKRKIARDEGKAFPKGAMSVNLKMGAFVLYLVDL 295
DB 263 TSGEA---VKYSSFEGRQLLAKEGARSFPGAGANILRGAAGVLSITYDQV 314

RESULT 15
ADT_CHLRE
ID ADT_CHLRE STANDARD: PRT: 308 AA.
AC P27080;
DT 01-AUG-1992 (rel. 23, Created)
DT 01-AUG-1992 (rel. 23, Last sequence update)
DT 01-OCT-1994 (rel. 30, Last annotation update)
DE ADP/ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE
DE TRANSLOCATOR) (ANT).
GN ABT.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

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Search completed: February 13, 2002, 09:34:43
Job time: 200 sec

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OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FUDA4-R2;
RX MEDLINE=93204867; PubMed=8455552;
RA Sharpe J.A., Day A.;
RT "Structure, evolution and expression of the mitochondrial ADP/ATP
   translocator gene from Chlamydomonas reinhardtii.";
RL Mol. Gen. Genet. 237:134-144(1993)
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
   MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
   INNER MEMBRANE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC -----
CC EMBL: X65194; CAA46311.1; -
CC PIR: S30259; S30259.
CC InterPro: IPR002067; Mit_Carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carri: 3.
CC PRINTS: PRO0926; MITOCARRIER.
CC PRINTS: PRO0927; ADPTRNSLCASE.
CC PROSITE: PS00215; MITOCH_CARRIER; 2.
CC Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport.
KM TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 74 92 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 178 197 4 (POTENTIAL).
FT TRANSMEM 217 234 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
SQ SEQUENCE 308 AA; 33528 MW; D477CFDE72B7A53F CRC64;

Query Match 49.5%; Score 765; DB 1; Length 308:
Best Local Similarity 52.6%; Pred. No. 5.8e-61;
Matches 159; Conservative 49; Mismatches 78; Indels 16; Gaps 6;

OY 7 SFAPKDLAGVAAAIKTAAPVPIERVKLLIQV-HASKQITADKQYGIIDCVIRPKEQ 65
   :| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 7 NFWDVFLAGLSAAVSKTAAPVPIERVKLLIQNDDEMIKQGRSLAPYKIGECFVRTVEE 66

OY 66 EVLSFWNGNLANYIRYPPQALNPAFKDKYKQIFLGVDKRTQFWRVFAGNLASGAGA 125
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 67 GFSGLMRGNTANYIRIFPTQALNPAFKDKRRMF--GFNKKDEYKWFAGMASGAGA 124

OY 126 TSLCFVYPLDFARTRLAAD--VGKACAREFRGLGDLVKYKSDGKIGLYOGFNVSVQ 182
   || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 125 VSLSEFVSLDYARTRLANDAKSAKKGGRQFNGLVYRRTIASDGIAGLYRGFNISCV 184

OY 183 GIIIRAAVFGIYDTANG-HLPDPKNTHIYISMMIAQTVTAAGLTSPEDTVARRMMQ 241
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 185 GIIVYRGLYFGMDLKLPPVGLVGLANNFLAFLGLGWTIGAGLASYPIDTIRRRMMT 244

OY 242 SGRGTDIMTGTLDGCRKLTARDEGKAFKGAWSNVLRGMGAFAVLVLYDEI-----K 295
   | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |
DB 245 S---GSAVKYNSRHCQEIYKKNBGMKSLFKGAGANILRAVAGAGVLAGYDQLGVILLGK 301

OY 296 KY 297
   ||
DB 302 KY 303
```


GenCore version 4.5
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OW protein - protein search, using sw model

Run on: February 13, 2002, 09:32:07 ; Search time 34.78 Seconds

(without alignments)
652.674 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDALSPAKDFLAGVAAA.....LRGMGARFVLVDEIRKVT 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapept 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

1: PIR_68:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1547	100.0	298	1 A29132	ADP,ATP carrier pr
2	1479	95.6	298	2 S31814	ADP,ATP carrier pr
3	1458	94.2	298	2 B43646	ADP,ATP carrier pr
4	1454	94.0	298	1 S03894	ADP,ATP carrier pr
5	1419	91.7	298	1 XMBO	ADP,ATP carrier pr
6	1417	91.6	298	2 S37210	ADP,ATP carrier pr
7	1417	91.6	298	2 160173	adenine nucleotide
8	1413	91.3	298	1 A44778	ADP,ATP carrier pr
9	1170	73.6	301	1 S31935	ADP,ATP carrier pr
10	1032	66.7	300	2 T23571	hypothetical prote
11	1029	66.5	313	2 T23207	hypothetical prote
12	1029	66.5	313	2 T25850	hypothetical prote
13	986	63.7	300	2 T15206	hypothetical prote
14	968	62.6	339	2 A41677	ADP,ATP carrier pr
15	938	60.6	301	2 S51132	ADP,ATP carrier pr
16	771	49.8	386	2 T09709	ADP,ATP carrier pr
17	770	49.8	322	2 T40526	ADP,ATP carrier pr
18	765	49.5	308	1 S30259	ADP,ATP carrier pr
19	761.5	49.2	307	2 A36582	ADP,ATP carrier pr
20	759	49.1	326	2 T25728	hypothetical prote
21	759	49.1	387	2 S14876	ADP,ATP carrier pr
22	757	48.9	313	1 XMWC	ADP,ATP carrier pr
23	754	48.7	386	2 S17917	ADP,ATP carrier pr
24	753	48.7	387	2 S16568	ADP,ATP carrier pr
25	752.5	48.6	318	1 A31978	ADP,ATP carrier pr
26	752	48.6	386	2 S21974	ADP,ATP carrier pr
27	749.5	48.4	305	2 S68154	ADP,ATP carrier pr
28	749.5	48.4	306	2 T20012	hypothetical prote
29	746	48.2	306	2 T42011	ADP,ATP carrier pr

30	746	48.2	379	2 T04608	ADP,ATP carrier pr
31	745.5	48.2	385	1 S29852	ADP,ATP carrier pr
32	745	48.2	382	2 S33630	ADP,ATP carrier pr
33	741.5	47.9	379	2 S21313	ADP,ATP carrier pr
34	741.5	47.9	386	2 S14874	ADP,ATP carrier pr
35	728	47.1	298	2 A24849	ADP,ATP carrier pr
36	665.5	43.0	298	2 T24029	hypothetical prote
37	521.5	33.7	327	2 T51577	ADP/ATP translocas
38	388	25.1	325	2 T04273	ADP/ATP translocas
39	372	24.0	381	2 T51158	hypothetical prote
40	372	24.0	415	2 T48171	hypothetical prote
41	356	23.0	352	2 T01729	hypothetical prote
42	350	22.6	475	2 T50686	mitochondrial solu
43	340	22.0	358	2 T45934	peroxisomal Ca-dep
44	334	21.6	348	2 D84798	hypothetical prote
45	322.5	20.8	332	2 T47703	probable mitochond
					Ca-dependent solut

ALIGNMENTS

RESULT 1

A29132
ADP,ATP carrier protein T2 - human
N:Alternate names: mitochondrial ADP,ATP translocase 2
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: A29132; C28116
R:Ballini, R.; Ferrari, S.; Kacmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
J. Biol. Chem. 262, 4355-4359, 1987
A>Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regu
A:Reference number: A29132; MUID:87160056
A:Accession: A29132
A:Molecule type: mRNA
A:Residues: 1-298 <BAT>
A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
R:Houldsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:88124845
A:Accession: C28116
A:Molecule type: mRNA
A:Residues: 47-65,'G',67-110,'L',112-161,'G',163-298 <HOU>
A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
A:Experimental source: clone pHAT3
C:Genetics:
A:Gene: GDB:ANT2; T3; 2P1
A:Cross-references: GDB:125190; OMIM:300150
A:Map position: Xq13-Xq26
A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 100.0%; Score 1547; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 2e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAAISTRAVAPTEVRKLLLOVHASKOITADKOVGIIDCVR 60
DB 1 MTDALSPAKDFLAGVAAAISTRAVAPTEVRKLLLOVHASKOITADKOVGIIDCVR 60
QY 61 IPKQEVLSFMRGNLANVIRFFPQALNFARFKDKYKQIFLGVNKRQOFWYFPGNLASG 120
DB 61 IPKQEVLSFMRGNLANVIRFFPQALNFARFKDKYKQIFLGVNKRQOFWYFPGNLASG 120
QY 121 GAACATSLCEVYPLDFAFRTRLADVYKAGAEERERGLGDCLVKTKYKSGIKGLYGFNVS 180
DB 121 GAACATSLCEVYPLDFAFRTRLADVYKAGAEERERGLGDCLVKTKYKSGIKGLYGFNVS 180

OY 181 VGGIITRYRAAYGIVDTAKGMLPDPKNTHTIVISMIAQTAVAGLTSYFPDTRRRMM 240
 |||
 Db 181 VGGIITRYRAAYGIVDTAKGMLPDPKNTHTIVISMIAQTAVAGLTSYFPDTRRRMM 240
 |||
 OY 241 QSGRKGTDTIMYGTLDCKWKRIARDEGKAFKFGAMSNVLRGMGAFVLVLYDEIKRYT 298
 |||
 Db 241 QSGRKGTDTIMYGTLDCKWKRIARDEGKAFKFGAMSNVLRGMGAFVLVLYDEIKRYT 298
 |||

RESULT 2

S31814

ADP,ATP carrier protein T2 - mouse

N:Alternate names: adenine nucleotide translocase

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998

C:Accession: S31814

R:Costet, P.; Laplace, C.

Submitted to the EMBL Data Library, January 1993

A:Reference number: S31814

A:Accession: S31814

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <COS>

A:Cross-references: EMBL:X70847

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 95.6%; Score 1479; DB 2; Length 298;
 Best Local Similarity 95.6%; Pred. No. 2.1e-123;
 Matches 285; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTDALISFAKDFLAGVAAIAISTAVAPIERVYKLLIQVHASKQITADKQYKIIDCVVR 60
 |||
 Db 1 MTDAAVSFAKDFLAGVAAIAISTAVAPIERVYKLLIQVHASKQITADKQYKIIDCVVR 60
 |||
 OY 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRFRYAGNLAAG 120
 |||
 Db 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRFRYAGNLAAG 120
 |||
 OY 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFRLGDLVYKISDGIKLYGFNVS 180
 |||
 Db 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFRLGDLVYKISDGIKLYGFNVS 180
 |||
 OY 181 VGGIITRYRAAYGIVDTAKGMLPDPKNTHTIVISMIAQTAVAGLTSYFPDTRRRMM 240
 |||
 Db 181 VGGIITRYRAAYGIVDTAKGMLPDPKNTHTIVISMIAQTAVAGLTSYFPDTRRRMM 240
 |||
 OY 241 QSGRKGTDTIMYGTLDCKWKRIARDEGKAFKFGAMSNVLRGMGAFVLVLYDEIKRYT 298
 |||
 Db 241 QSGRKGTDTIMYGTLDCKWKRIARDEGKAFKFGAMSNVLRGMGAFVLVLYDEIKRYT 298
 |||

RESULT 3

B43646

ADP,ATP carrier protein T2 - bovine

C:Species: Bos primigenius taurus (catle)

C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999

C:Accession: B43646

R:Powell, S.J.; Mead, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in

A:Reference number: A43646; MUID:89229093

A:Accession: B43646

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <POM>

A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1458; DB 2; Length 298;
 Best Local Similarity 92.9%; Pred. No. 1.5e-121;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

OY 1 MTDALISFAKDFLAGVAAIAISTAVAPIERVYKLLIQVHASKQITADKQYKIIDCVVR 60
 |||
 Db 1 MTEQALISFAKDFLAGVAAIAISTAVAPIERVYKLLIQVHASKQITADKQYKIIDCVVR 60
 |||
 OY 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRFRYAGNLAAG 120
 |||
 Db 61 IPKEQEVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRFRYAGNLAAG 120
 |||
 OY 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFRLGDLVYKISDGIKLYGFNVS 180
 |||
 Db 121 GAAGATSLCFVYPLDFARTRLAADVAGKAGAREFRLGDLVYKISDGIKLYGFNVS 180
 |||
 OY 181 VGGIITRYRAAYGIVDTAKGMLPDPKNTHTIVISMIAQTAVAGLTSYFPDTRRRMM 240
 |||
 Db 181 VGGIITRYRAAYGIVDTAKGMLPDPKNTHTIVISMIAQTAVAGLTSYFPDTRRRMM 240
 |||
 OY 241 QSGRKGTDTIMYGTLDCKWKRIARDEGKAFKFGAMSNVLRGMGAFVLVLYDEIKRYT 296
 |||
 Db 241 QSGRKADIMYGTVDCKWKRIARDEGKAFKFGAMSNVLRGMGAFVLVLYDELKRYT 296
 |||

RESULT 4

S03894

ADP,ATP carrier protein T3 - human

N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,

C:Species: Homo sapiens (man)

C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: S03894; B28116

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP

A:Reference number: S03893; MUID:89236396

A:Accession: S03894

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <COZ>

R:Houldsworth, J.; Altardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in

A:Reference number: A94197; MUID:88124845

A:Accession: B28116

A:Molecule type: mRNA

A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOU>

A:Cross-references: GB:J03592; NID:9339722; PIDN:AAA6750.1; PID:9339723

A:Experimental source: liver

C:Genetics:

A:Gene: GDB:ANT3; ANT3Y

A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.0%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 3.4e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTDALISFAKDFLAGVAAIAISTAVAPIERVYKLLIQVHASKQITADKQYKIIDCVVR 60
 |||
 Db 1 MTDALISFAKDFLAGVAAIAISTAVAPIERVYKLLIQVHASKQITADKQYKIIDCVVR 60
 |||

Db 1 MTEQALSFADKFLAGGIAAISTAVAPIERVKLLLOVQHASKOIADKQYGIIDCVR 60
QY 1 IPKEQEVLSFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDYKROQFMRFGNLSG 120
Db 61 IPKEQGLSLFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDYKROQFMRFGNLSG 120
QY 121 GAAGATSLCFYVPLDFAFTRTLAADVKGAGAREFERGLDCLVKIKYSDGIGLYOGFNV 180
Db 121 GAAGATSLCFYVPLDFAFTRTLAADVKGAGAREFERGLDCLVKIKYSDGIGLYOGFNV 180
QY 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIYSWMIAGTAVAGLTSYPEDTVRRMM 240
Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIYSWMIAGTAVAGLTSYPEDTVRRMM 240
QY 241 OSGRKGDIMYTGTLDCWKRIARDEGKAFKFGAMSNVLRMGGAFLVLYDEIKK 296
Db 241 OSGRKGDIMYTGTLDCWKRIARDEGKAFKFGAMSNVLRMGGAFLVLYDEIKK 296

RESULT 5
XMB0
ADP,ATP carrier protein T1 - bovine
N:Alternate names: ADP/ATP translocase T1
C:Species: Bos primigenius taurus (cattle)
C>Date: 14-Nov-1983 #sequence,revision 22-Jul-1994 #text_change 22-Jun-1999
C:Accession: A43646; A24822; A03181; A61343; S69369
R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
BiochemJ 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A:Reference number: A43646; M0ID:89229093
A:Accession: A43646
A:Molecule type: mRNA
A:Residues: 1-298 <POM>
A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415
R:Rasmussen, U.B.; Wohlrab, H.
Biochem. Biophys. Res. Commun. 138, 850-857, 1986
A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
A:Reference number: A24822; M0ID:86295775
A:Accession: A24822
A:Molecule type: mRNA
A:Residues: 208-298 <RAS>
A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
R:Aquila, H.; Miera, D.; Eulitz, M.; Kilgenberg, M.
Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
A:Reference number: A03181; M0ID:82188267
A:Accession: A03181
A:Molecule type: protein
A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <ADU>
A:Note: residue 52 may be methyllysine
R:Babel, W.; Wachter, E.; Aquila, H.; Kilgenberg, M.
Biochim. Biophys. Acta 670, 176-180, 1981
A:Title: Amino acid sequence determination of the ADP,ATP carrier from beef heart mitochondrion
A:Reference number: A61343; M0ID:82046808
A:Accession: A61343
A:Molecule type: protein
A:Residues: 205-298 <BAB>
R:Oetmeier, W.; Masson, K.; Kalina, S.
Eur. J. Biochem. 227, 730-733, 1995
A:Title: [(3H)-7-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
A:Reference number: S69369; M0ID:95172058
A:Accession: S69369
A:Molecule type: protein
A:Residues: 49-63:154-168 <OET>
C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
C:Complex: homodimer
C:Function:
A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
A:Note: located in the inner mitochondrial membrane
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitochon
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 91.7%; Score 1419; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 4,36-118;
Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGGVAIAISKTAVAPIERVKLLLOVQHASKOITADKQYGIIDCVR 60
Db 1 MSDQALSLFKDFLAGGVAIAISKTAVAPIERVKLLLOVQHASKOISAEKQYGIIDCVR 60
QY 61 IPKEQEVLSFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDYKROQFMRFGNLSG 120
Db 61 IPKEQGLSLFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDYKROQFMRFGNLSG 120
QY 121 GAAGATSLCFYVPLDFAFTRTLAADVKGAGAREFERGLDCLVKIKYSDGIGLYOGFNV 180
Db 121 GAAGATSLCFYVPLDFAFTRTLAADVKGAGAREFERGLDCLVKIKYSDGIGLYOGFNV 180
QY 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIYSWMIAGTAVAGLTSYPEDTVRRMM 240
Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIYSWMIAGTAVAGLTSYPEDTVRRMM 240
QY 241 OSGRKGDIMYTGTLDCWKRIARDEGKAFKFGAMSNVLRMGGAFLVLYDEIKK 297
Db 241 OSGRKGDIMYTGTLDCWKRIARDEGKAFKFGAMSNVLRMGGAFLVLYDEIKK 297

RESULT 6
S37210
ADP,ATP carrier protein T1 - mouse
N:Alternate names: adenine nucleotide carrier
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence,revision 06-Jan-1995 #text_change 20-Aug-1999
C:Accession: S37210
R:Laplace, C.; Costel, P.
submitted to the EMBL Data Library, September 1993
A:Reference number: S37210
A:Accession: S37210
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-298 <LAP>
A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
C:Genetics:
A:Gene: ANCL1
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 91.6%; Score 1417; DB 2; Length 298;
Best Local Similarity 89.6%; Pred. No. 6,56-118;
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDAAISFAKDFLAGGVAIAISKTAVAPIERVKLLLOVQHASKOITADKQYGIIDCVR 60
Db 1 MGDQALSLFKDFLAGGVAIAISKTAVAPIERVKLLLOVQHASKOISAEKQYGIIDCVR 60
QY 61 IPKEQEVLSFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDYKROQFMRFGNLSG 120
Db 61 IPKEQGLSLFWRGNLANVIRFPFOALNFAFKDKYKQIFLGVDYKROQFMRFGNLSG 120
QY 121 GAAGATSLCFYVPLDFAFTRTLAADVKGAGAREFERGLDCLVKIKYSDGIGLYOGFNV 180
Db 121 GAAGATSLCFYVPLDFAFTRTLAADVKGAGAREFERGLDCLVKIKYSDGIGLYOGFNV 180
QY 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIYSWMIAGTAVAGLTSYPEDTVRRMM 240
Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIYSWMIAGTAVAGLTSYPEDTVRRMM 240

A:Accession: S31935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-301 <BE>
A:Cross-references: EMBL:Z21814; EMBL:Z21815
C:Keywords: ADP, ATP carrier protein; ADP, ATP carrier protein; duplication; transmembrane protein
E:7-101/Domain: ADP, ATP carrier protein repeat homology <ACP1>
E:112-204/Domain: ADP, ATP carrier protein repeat homology <ACP2>
E:209-300/Domain: ADP, ATP carrier protein repeat homology <ACP3>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:33:11 ; Search time 57.26 Seconds
(without alignments)
385.502 Million cell updates/sec

Title: US-09-393-441-32

Perfect score: 1547

Sequence: 1 MTDAALSFANDFLAGVAAA.....LRGMAFVLVLEIKKYYT 298

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_1101:*

- 1: /SIDS8/gcgdata/geneseq/AA1980.DAT:*
- 2: /SIDS8/gcgdata/geneseq/AA1981.DAT:*
- 3: /SIDS8/gcgdata/geneseq/AA1982.DAT:*
- 4: /SIDS8/gcgdata/geneseq/AA1983.DAT:*
- 5: /SIDS8/gcgdata/geneseq/AA1984.DAT:*
- 6: /SIDS8/gcgdata/geneseq/AA1985.DAT:*
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- 10: /SIDS8/gcgdata/geneseq/AA1989.DAT:*
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- 13: /SIDS8/gcgdata/geneseq/AA1992.DAT:*
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- 18: /SIDS8/gcgdata/geneseq/AA1997.DAT:*
- 19: /SIDS8/gcgdata/geneseq/AA1998.DAT:*
- 20: /SIDS8/gcgdata/geneseq/AA1999.DAT:*
- 21: /SIDS8/gcgdata/geneseq/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1547	100.0	298	21	AAV71032
2	1547	100.0	298	22	AAU01199
3	1454	94.0	298	21	AAV71033
4	1454	94.0	298	22	AAW39641
5	1454	94.0	298	22	AAU01200
6	1454	94.0	323	22	AAW41427
7	1411	91.2	298	19	AAW61169
8	1391.5	89.9	297	21	AAV71031
9	1391.5	89.9	297	22	AAU01198
10	747.5	48.3	346	21	AAW37261
11	747.5	48.3	346	21	AAW37261

12	747.5	48.3	346	21	AAW37264	Arabidopsis thaliana
13	747.5	48.3	346	21	AAW38460	Arabidopsis thaliana
14	747.5	48.3	363	21	AAW36576	Arabidopsis thaliana
15	747.5	48.3	363	21	AAW37260	Arabidopsis thaliana
16	747.5	48.3	363	21	AAW37263	Arabidopsis thaliana
17	747.5	48.3	363	21	AAW38459	Arabidopsis thaliana
18	747.5	48.3	381	21	AAW36575	Arabidopsis thaliana
19	747.5	48.3	381	21	AAW37259	Arabidopsis thaliana
20	747.5	48.3	381	21	AAW37262	Arabidopsis thaliana
21	747.5	48.3	381	21	AAW38458	Arabidopsis thaliana
22	747.5	48.3	992	21	AAW38672	Arabidopsis thaliana
23	747.5	48.3	1009	21	AAW38671	Arabidopsis thaliana
24	747.5	48.3	1027	21	AAW38670	Arabidopsis thaliana
25	744.5	48.1	346	21	AAW17731	Arabidopsis thaliana
26	744.5	48.1	363	21	AAW17730	Arabidopsis thaliana
27	744.5	48.1	381	21	AAW17729	Arabidopsis thaliana
28	741.5	47.9	386	22	AAW00106	ADP/ATP carrier pr
29	690.5	44.6	330	21	AAW39398	Arabidopsis thaliana
30	687.5	44.4	330	21	AAW20658	Arabidopsis thaliana
31	687.5	44.4	333	21	AAW06857	Arabidopsis thaliana
32	687.5	44.4	350	21	AAW06856	Arabidopsis thaliana
33	687.5	44.4	368	21	AAW06855	Arabidopsis thaliana
34	660.5	42.7	291	21	AAW39399	Arabidopsis thaliana
35	657.5	42.5	291	21	AAW20659	Arabidopsis thaliana
36	655	42.3	306	21	AAW12916	Arabidopsis thaliana
37	655	42.3	306	21	AAW16974	Arabidopsis thaliana
38	637	41.2	291	21	AAW12917	Arabidopsis thaliana
39	637	41.2	291	21	AAW16975	Arabidopsis thaliana
40	585.5	37.8	249	21	AAW39400	Arabidopsis thaliana
41	582.5	37.7	249	21	AAW20660	Arabidopsis thaliana
42	574.5	37.1	312	21	AAW28188	Arabidopsis thaliana
43	570.5	36.9	263	21	AAW12918	Arabidopsis thaliana
44	570.5	36.9	263	21	AAW16976	Arabidopsis thaliana
45	565.5	36.6	228	21	AAW28189	Arabidopsis thaliana

ALIGNMENTS

RESULT 1	
ID	AAV71032 standard; Protein: 298 AA.
AC	AAV71032;
XX	
DT	29-AUG-2000 (first entry)
XX	
DE	Human adenine nucleotide translocator ANT2.
XX	
KW	Human: adenine nucleotide translocator: ANT2; mitochondria: ADP: ATP;
KW	adenosine di-phosphate: adenosine tri-phosphate: apoptosis: MPT: cancer;
KW	mitochondrial permeability transition; neuroprotective; neurotropic;
KW	antiparkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
KW	antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW	diabetes: Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;
KW	myoclonic epilepsy red ragged fibre syndrome.
XX	
OS	Homo sapiens.
XX	
PN	MO200026370-A2.
XX	
PD	11-MAY-2000.
XX	
PF	03-NOV-1999; 99WO-US25883.
XX	
PR	03-NOV-1998; 98US-0185904.
XX	
PR	08-SEP-1999; 99US-0393441.
XX	
PA	(MITO-) MITOKOR.
XX	

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,
 PI Ghosh SS;
 DR MPI: 2000-365619/31.
 DR N-PSDB: AAD00520.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 45; Page 172-173; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX
 SO Sequence 298 AA:
 Query Match 100.0%; Score 1547; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1,1e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFKDDPLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYGIIDCVR 60
 DB 1 mtdaalstfkdllagvaaaistavapieryklllyqghaskqiltadqygiidcvr 60
 QY 61 IPKEQEVLSFMWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 ipkegevlstfwrnglanvlyrptqalnfafkdkyqiflgvdkrftwryfagnlasg 120
 QY 121 GAAGATSLCFVVPDLPFARTRLAADVKGAGAEFRGCLDCLVKIKYKSDGINKLYOGFNVS 180
 DB 121 gaagatslcfvvpdlpfartrlaadvkgagaeefrgclclvkikysdginklyogfnvs 180
 QY 181 VGGIITVRAAYFGIVDTAGKMLPDKRNTHIVISWMAQVTVAVAGTSTPPTVRRMM 240
 DB 181 vggiiitvraayfgivdtakgmldpdknthivismwagvtvavagltspftvrrmm 240
 QY 241 GSGRGTDMYGTGLDQWKRKIADEGKAFKFGAMSNVLRGGAFAVLVLYDEIRKKT 298
 DB 241 gsgrgtdlmygtglcdwkrkiardegkafkfgamsnvlrsggafvlylydeirkkt 298

RESULT 2
 ID AAU01199 standard; Protein; 298 AA.
 AC AAU01199;
 XX
 DT 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX.

OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelebi G, Davis RE;
 DR MPI: 2001-291054/30.
 DR N-PSDB: AAS05902.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure: Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SO Sequence 298 AA:
 Query Match 100.0%; Score 1547; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1,1e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSFKDDPLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYGIIDCVR 60
 DB 1 mtdaalstfkdllagvaaaistavapieryklllyqghaskqiltadqygiidcvr 60
 QY 61 IPKEQEVLSFMWGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRYFAGNLASG 120
 DB 61 ipkegevlstfwrnglanvlyrptqalnfafkdkyqiflgvdkrftwryfagnlasg 120
 QY 121 GAAGATSLCFVVPDLPFARTRLAADVKGAGAEFRGCLDCLVKIKYKSDGINKLYOGFNVS 180
 DB 121 gaagatslcfvvpdlpfartrlaadvkgagaeefrgclclvkikysdginklyogfnvs 180
 QY 181 VGGIITVRAAYFGIVDTAGKMLPDKRNTHIVISWMAQVTVAVAGTSTPPTVRRMM 240
 DB 181 vggiiitvraayfgivdtakgmldpdknthivismwagvtvavagltspftvrrmm 240
 QY 241 GSGRGTDMYGTGLDQWKRKIADEGKAFKFGAMSNVLRGGAFAVLVLYDEIRKKT 298
 DB 241 gsgrgtdlmygtglcdwkrkiardegkafkfgamsnvlrsggafvlylydeirkkt 298

RESULT 3
 ID AAY71033 standard; Protein; 298 AA.
 XX AAY71033:
 XX 29-AUG-2000 (first entry)
 DT
 DE Human adenine nucleotide translocator ANT3.
 XX
 KM Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; cancer;
 KM mitochondrial permeability transition; neuroprotective; nootropic;
 KM antiParkinsonian; cyostatic; antidiabetic; anticonvulsant; neuroleptic;
 KM antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 XX
 OS Homo sapiens.
 XX
 PN W0200026370-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99MO-US25883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR WPI; 2000-365619/31.
 DR N-PSDB; AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 PS Claim 46; Page 173-174; 175pp; English.
 XX
 XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 XX
 Sequence 298 AA:

Query Match	94.0%	Score 1454;	DB 21;	Length 298;
Best Local Similarity	92.6%;	Pred. NO.	7e-145;	
Matches 274; Conservative	13;	Mismatches	9;	Indels 0; Gaps 0
OY	1	MTDALSFRAKDELACGVAALISKTAVAPERKKLLQOVHASKQTADPKOYKGIIDCVNR	60	
	:	:	:	:

Db	1	mtbeaistefakfflaggliaaaistcaavpiervkllllqvghaskbjaadckgkylgvdcivr	60
Qy	61	IPKDEOELSPWKGMLANVIYRPYQALNFAFKDKYKQIPLFGVDKRTQFMWRFEAGNLASC	120
Db	61	ipkeqvysfwrnlanviryfpcqalnafekdkykgiflgvdkhceqfwryfaglnasg	120
Qy	121	GAACATSLCFWYRPIDFAPRTLRALAAVNGKAGARERFGIGDCLVYKTKSDGIKGLQGPNVS	180
Db	121	gaagatsctcypldfactarlaaavngsksterefrlgdcvtkltskdsdglrglyqgfsvs	180
Qy	181	VQGIIRAAAFYGLIDPAKAGMLPDPKNTHTIYISMMIAQTYAAVAGLSTSPEDTVRRRMM	240
Db	181	vqglliyraayfygyldcakgmllpdpknthtlvsvsmiaqvtvavagvsypddtvtrrrrmm	240
Qy	241	QSGRKGDIMTGTGLDCRKRITARBEGGKAPFKGMSNVLRKMGCAFVLVLYLDELKK	296
Db	241	qsgrtkgsadimvtgcvdcwrklfrdeggskafkfgwmsvnlrsmggaftvlvlyldelkk	296

RESULT	4
AAM39641	ID AAM39641 standard; Protein; 298 AA.
AC	AAM39641;
DT	22-OCT-2001 (first entry)
DE	Human polypeptide SEQ ID NO 2786.
KW	Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.
OS	Homo sapiens.
PN	WO200153312-A1.
PD	26-JUL-2001.
PF	26-DEC-2000; 2000MC-US34263.
PR	21-JAN-2000; 2000US-0488725. 25-APR-2000; 2000US-0552317. 09-JUL-2000; 2000US-0598042. 19-JUL-2000; 2000US-0620312. 03-AUG-2000; 2000US-0653450. 14-SEP-2000; 2000US-0662191. 19-OCT-2000; 2000US-0693036. 29-NOV-2000; 2000US-0727344.
PA	(HYSE-) HYSEQ INC.
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J; Zhao QA, Zhou P, Goodrich R, Drmanac RT;
DR	WPI: 2001-442253/47. N-PSDB: AA158797.
PT	Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
XX	Example 4: SEQ ID NO 2786; 10078bp; English.
CC	The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 298 AA:

Query Match 94.0%; Score 1454; DB 22; Length 298;

Best Local Similarity 92.6%; Pred. No. 7e-145;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSEAKDFLAGVAAIAISKTAAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 DB 1 mdegaisfakdfiaaglaaistkavapiervkllqvhaskqiaadkqyqivdcivr 60
 QY 61 IPKEDEVLSFMRGNLANVIRFPTQALNFAFDKQKQIFLGVDKRTQPMRFAGNLASG 120
 DB 61 IPKEGVLSFMRGNLANVIRFPTQALNFAFDKQKQIFLGVDKRTQPMRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFRGLDCLVKIKYKSDGIKLYGPFNV 180
 DB 121 gaagatslcfvypldfartrlaadvgksqterefrglgclvklksdglgylgfsvs 180
 QY 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTNIVSWMIAQVTAVAGLTSYPTPTVRRMM 240
 DB 181 vggiliryaaifgyvdtakgmldpdknthiivswmlaqvtavagvsvptfvtvrrmm 240
 QY 241 GSGRKGTDMVYGTLDCKRKIARDEGKAFFKGAMSNVLRGGAFLVLYDEIK 296
 DB 241 gsgrrgtldmvygtldckrkiaardegkaffkgamsnvlrnggafvlvlydeik 296

RESULT 5

AAU01200 standard; Protein; 298 AA.

AC AAU01200;

DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-3 (ANT-3) protein.

XX Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.

PN WO200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000MO-US30535.

PR 03-NOV-1999; 99US-0434354.

PA (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;

PI Vellcelebdi G, Davis RE;

DR WPI; 2001-291054/30.

DR N-PSDB; AAS05903.

PT New nucleic acid expression constructs, useful for screening for agents

PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -

PS Disclosure: Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

SQ Sequence 298 AA:

Query Match 94.0%; Score 1454; DB 22; Length 298;

Best Local Similarity 92.6%; Pred. No. 7e-145;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDALSEAKDFLAGVAAIAISKTAAPIERVKLLQVOHASKQTADKQYKGIIDCVVR 60
 DB 1 mdegaisfakdfiaaglaaistkavapiervkllqvhaskqiaadkqyqivdcivr 60
 QY 61 IPKEDEVLSFMRGNLANVIRFPTQALNFAFDKQKQIFLGVDKRTQPMRFAGNLASG 120
 DB 61 IPKEGVLSFMRGNLANVIRFPTQALNFAFDKQKQIFLGVDKRTQPMRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFRGLDCLVKIKYKSDGIKLYGPFNV 180
 DB 121 gaagatslcfvypldfartrlaadvgksqterefrglgclvklksdglgylgfsvs 180
 QY 181 VGGIIIRAAVFGIYDTAKGMLPDPKNTNIVSWMIAQVTAVAGLTSYPTPTVRRMM 240
 DB 181 vggiliryaaifgyvdtakgmldpdknthiivswmlaqvtavagvsvptfvtvrrmm 240
 QY 241 GSGRKGTDMVYGTLDCKRKIARDEGKAFFKGAMSNVLRGGAFLVLYDEIK 296
 DB 241 gsgrrgtldmvygtldckrkiaardegkaffkgamsnvlrnggafvlvlydeik 296

RESULT 6

AA41427 standard; Protein; 323 AA.

AC AA41427;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6358.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

XX peripheral nervous system; neuropathy; central nervous system; CNS;

XX Alzheimer's, Parkinson's disease, Huntington's disease; haemostatic;

XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

XX leukaemia.

XX Homo sapiens.

PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
DR N-PSDB: AA160383.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Example 2; SEQ ID NO 6358; 10078bp; English.
PS
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA38642-AA42213) with nootropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 323 AA:
SQ
Query Match 94.0%; Score 1454; DB 22; Length 323;
Best Local Similarity 92.6%; Pred. No. 7.8e-145;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
OY 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYGIIDCVR 60
DB ||:||||||||||||||||||||||||||||||||||||||||||||||||||
26 mteqalsfakdfliagsglaaaisktavapiervklllqvghaskqjlaadkqygiidcvr 85
OY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVVKRQOFMFYFAGNLASG 120
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||||||
86 lpeqgylstfwrqnlavirlyfpcqalnfaikdkyqkflfgvavkhqfwyafagnlasg 145
OY 121 GAAGATSLCFVYPLDFAFTRILADVKGAGAEERFERGLDCLVKYKSDGIGLYOGFNVS 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||
146 gaagatslcfvypldfartcllaadvkgsqterefrgldclvkltskdglrtqlyqgfsvs 205
OY 181 VQGIIRRAAYFGIYDTAKGMLPDKMTHIVISMIAQVTAAGLTSYPEYTVRRMM 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||
206 vqglllytraayfgvydtkamlpdkmthlvswsmiaqvcvavagvsvyptdvtvrrmm 265
OY 241 QSGKRGDIWYTGFLDCWRKILARDEGKAPFKGAMSVNLRMGCAFVLVYDETIK 296
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||
266 qsgkrgedimyltgcwdrkllrdeggkalfkgasvnlrtgmgaftvlyvdelk 321

RESULT 7
AAW61169
ID AAW61169 standard; Protein: 298 AA.
XX
XX AAW61169;
AC
XX
XX 28-SEP-1998 (first entry)
DT
XX
XX
DE Anti protein.
XX
XX Anti; Adenine nucleotide translocator; cloning; screening;
KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe: OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
XX
XX Mus sp.
OS
XX
XX WO9819714-A1.
PN
XX
XX 14-MAY-1998.
PD
XX
XX 31-OCT-1997; 97WO-US19882.
PF
XX
XX 01-NOV-1996; 96US-0030017.
PR
XX
XX (UYEM-) UNIV EMORY.
PA
XX
XX Graham BC, Macgregor GR, Wallace DC;
PI
XX
XX WPI: 1998-286608/25.
DR N-PSDB: AAV36479.
XX
XX Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
XX Disclosure; Page 39-40; 61pp; English.
PS
XX
XX The present sequence is the mouse Anti protein, the cDNA producing this
CC polypeptide is cloned by screening a mouse heart cDNA library with the
CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA
CC Tag dideoxy terminator cycle sequencing. The Anti protein is encoded by
CC the Anti locus, a nuclear gene on chromosome 8. This protein is required
CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
CC which can then be converted into ATP. An Anti homozygous mutant would
CC thus be defective in OXPHOS which results in disease in oxidative
CC metabolism dependent tissues. This mouse Anti homozygous mutant can be
CC used as a model system for fascioscapular humeral muscular dystrophy.
CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
CC systems can be used to test possible therapeutic compounds which
CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
CC independent of ANTI.
XX
XX Sequence 298 AA:
SQ
Query Match 91.2%; Score 1411; DB 19; Length 298;
Best Local Similarity 89.2%; Pred. No. 2.4e-140;
Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
OY 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVQHSKQITADKQYGIIDCVR 60
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||
1 mtdaalsfakdfliagsglaaaisktavapiervklllqvghaskqjlaadkqygiidcvr 60
OY 61 IPKEQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVVKRQOFMFYFAGNLASG 120
DB ||||| ||||||||||||||||||||||||||||||||||||||||||||
61 ipkeqgylstfwrqnlavirlyfpcqalnfaikdkyqkflfgvavrhqfwyafagnlasg 120
OY 121 GAAGATSLCFVYPLDFAFTRILADVKGAGAEERFERGLDCLVKYKSDGIGLYOGFNVS 180
DB ||||||||||||||||||||||||||||||||||||||||||||

Db 121 gaagatslcfvypldfartrllaadvkgsqsfefnglgcliklfksdglklyggfsvs 180
 QY 181 VGGIIYRAAYGIVDTAKGMLPDPKNTHTIVISWMTAQTAVAGLTSPFPTVRRRMW 240
 Db 181 vggililyraayfgvydtkagmlpdpknvhlivswwlsgvtavagllsyplfdvttrmm 240
 QY 241 OSGRKGTDMYGTGLDCWKRRIARDEGKAFFKGAMSNVLRGAGFVLYDEIKKY 297
 Db 241 gsgrkgtadlmvgtlcvwrkklakdeganaeffkgawsnvlrgmgatvlylydeikky 297

RESULT 8
 AAY71031
 ID AAY71031 standard; Protein; 297 AA.
 AC AAY71031;
 XX
 DT 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator ANTL.
 XX
 KW Human: adenine nucleotide translocator; ANTL; mitochondria; ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; noctropic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antipsychotic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; KW mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200026370-A2.
 XX
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999; 99WO-US25883.
 XX
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 PA (MITO-) MITOKOR.
 PI
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR; Ghosh SS;
 PI
 XX WPI: 2000-365619/31.
 DR N-PSDB: AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator polypeptide, useful e.g. in screening for potential therapeutic agents against mitochondrial disease -
 PT
 XX
 PS Claim 44; Page 172; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator (ANT) proteins or ANT fusion proteins using recombinant expression constructs. ANT is a nuclear encoded protein and a major component of inner mitochondrial membrane. It mediates transport of adenosine di/tri-phosphates across the mitochondrial inner membrane and also serves as an important molecular component of the mitochondrial permeability transition pore, a modulator of apoptosis. ANT is used to identify agents or ligands that bind to, or interact with it. The ANT ligands are used to detect or isolate ANT in a biological sample, and therapeutically for regulating mitochondrial pore activity, for treating diseases associated with altered mitochondrial function, including Alzheimer's, Parkinson's and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red ragged fibre syndrome. The present sequence is an

CC adenine nucleotide translocator ANTL from human brain.
 XX
 SQ Sequence 297 AA:
 Query Match 89.9%; Score 1391.5; DB 21; Length 297;
 Best Local Similarity 88.6%; Pred. No. 2,7e-138;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSFAPKDFLAGVAATKSTAVAPLERKLLLOVNOHASKOITADBOYGGIIDCVVR 60
 Db 1 mgdhwstlkdlagavaavastlavaplerklllqvhnasqsaekyqxlldcavr 60
 QY 61 IPKEDEVLSEFWRGNLANVIRYPTQALNFAFDKYKQIFLAGVDKRTQPMRFAGNLASG 120
 Db 61 ipkegflsfwrgnlavirlyfptqalnfafdkyqqlflgvdvrtkqfwrfagnlsg 120
 QY 121 GAAGATSLCFVYPLDFARTRLLAADVGKAGAEERFGLSDCLVKYKSDGIKGLYGFNV 180
 Db 121 gaagatslcfvypldfartrllaadvgr-afrefnglgcliklfksdglrglyggfsvs 179
 QY 181 VGGIIYRAAYGIVDTAKGMLPDPKNTHTIVISWMTAQTAVAGLTSPFPTVRRRMW 240
 Db 181 vggililyraayfgvydtkagmlpdpknvhlivswwlsgvtavagllsyplfdvttrmm 239
 QY 241 OSGRKGTDMYGTGLDCWKRRIARDEGKAFFKGAMSNVLRGAGFVLYDEIKKY 297
 Db 241 gsgrkgtadlmvgtlcvwrkklakdegakafkgawsnvlrgmgatvlylydeikky 296

RESULT 9
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 AC AAU01198;
 XX
 DT 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-1 (ANT-1) protein.
 XX
 KW Human: adenine nucleotide translocator-1; ANT-1; MPT; cyclophilin; mitochondrial permeability transition pore component; cell survival; KW mitochondrial core component; mitochondrial related disorder; cancer; Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 KW
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 PF 03-NOV-1999; 99US-0434354.
 PR
 PA (MITO-) MITOKOR.
 PI
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG; Velicelebi G, Davis RE;
 PI
 XX WPI: 2001-291054/30.
 DR N-PSDB: AAS05901.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents that alter mitochondrial permeability transition (MPT), comprises polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused to energy transfer molecule -
 PT
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-1 (ANT-1) protein. ANT proteins are mitochondrial permeability transition (MPT) pore components responsible for mediating transport

PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144634.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0144816.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.

PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159337.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 48.3%; Score 747.5; DB 21; Length 346;
Best Local Similarity 53.9%; Pred. No. 2.3e-70;

Matches 166; Conservative 38; Mismatches 77; Indels 27; Gaps 8;

OY 7 SPFAKDLGVAVAIAISKTVAPIERVKLLVOVHASKQITA--DKQYGIIDCVVRIPK 63
DB 44 nfaIdfImgysaavksaavksaapierkvlllq--demikaglspeygidcfgrtlk 101
OY 64 EDEVLFSWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQWRFPAGNLAGSGAA 123
DB 102 deqfgslwtgrntanvirlyptqalnfaIdfkrlnfkfd-rdykwkfaqlaasgaa 160
OY 124 GATSLCEVYRPLDPARTRLAAD---VGKAGAREFRBGICVIVKYSDDGKIGYOGFNNS 180
DB 161 gassllfvySldyartclandakaakkggggrtfdgldvvyrtkltdglaqltgrfns 220
OY 181 VOGIITIRAAVFGIYDPAK----GMLPDPKNTNIVISMIAQTVYAVAGLTSYPTDVR 235
DB 221 cvglivtgrlyfsglvsavpalltfgldgSffasfalgwvI---tnglaslypidtr 276
OY 236 RRMWOSGRKRDIMTGTGLDCRKRTIARDEGGAFFPKGAMSNVLRGMCAPVLVLYDEI- 294
DB 277 rrmmtlsgaa--vkysldatfkqllknegaksltkgsaganllravagavlylsydklq 333
OY 295 -----KKY 297
DB 334 llvfgkky 341

RESULT 11
AAG37261
ID AAG37261 strand: Protein; 346 AA.
AC AAG37261;
XX 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 45788.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.

XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
PF 25-FEB-2000. 2000EP-0301439.
XX
XX 25-FEB-1999. 99US-0121825.
PR 05-MAR-1999. 99US-0123180.
PR 09-MAR-1999. 99US-0123548.
PR 23-MAR-1999. 99US-0125788.
PR 25-MAR-1999. 99US-0126264.
PR 29-MAR-1999. 99US-0126785.
PR 01-APR-1999. 99US-0127462.
PR 06-APR-1999. 99US-0128234.
PR 08-APR-1999. 99US-0128714.
PR 16-APR-1999. 99US-0129645.
PR 19-APR-1999. 99US-0130077.
PR 21-APR-1999. 99US-0130449.
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PR 30-APR-1999. 99US-0131449.
PR 30-APR-1999. 99US-0132048.
PR 04-MAY-1999. 99US-0132407.
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PR 01-JUN-1999. 99US-0137222.
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PR 04-JUN-1999. 99US-0137502.
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PR 17-JUN-1999. 99US-0139492.
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PR 18-JUN-1999. 99US-0139460.
PR 18-JUN-1999. 99US-0139461.
PR 18-JUN-1999. 99US-0139462.
PR 18-JUN-1999. 99US-0139463.
PR 18-JUN-1999. 99US-0139750.
PR 18-JUN-1999. 99US-0139750.
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PR 22-JUN-1999. 99US-0139899.
PR 23-JUN-1999. 99US-0140353.
PR 23-JUN-1999. 99US-0140354.
PR 24-JUN-1999. 99US-0140695.
PR 28-JUN-1999. 99US-0140823.
PR 29-JUN-1999. 99US-0140991.
PR 30-JUN-1999. 99US-0141287.

PR 01-JUL-1999. 99US-0141842.
PR 01-JUL-1999. 99US-0142154.
PR 02-JUL-1999. 99US-0142055.
PR 06-JUL-1999. 99US-0142380.
PR 08-JUL-1999. 99US-0142803.
PR 09-JUL-1999. 99US-0142920.
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PR 16-JUL-1999. 99US-0144086.
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PR 21-JUL-1999. 99US-0144814.
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PR 02-AUG-1999. 99US-0146389.
PR 03-AUG-1999. 99US-0147038.
PR 04-AUG-1999. 99US-0147204.
PR 04-AUG-1999. 99US-0147302.
PR 05-AUG-1999. 99US-0147192.
PR 05-AUG-1999. 99US-0147260.
PR 06-AUG-1999. 99US-0147303.
PR 06-AUG-1999. 99US-0147416.
PR 09-AUG-1999. 99US-0147493.
PR 09-AUG-1999. 99US-0147935.
PR 10-AUG-1999. 99US-0148171.
PR 11-AUG-1999. 99US-0148319.
PR 12-AUG-1999. 99US-0148341.
PR 13-AUG-1999. 99US-0148555.
PR 13-AUG-1999. 99US-0148684.
PR 16-AUG-1999. 99US-0149368.
PR 17-AUG-1999. 99US-0149175.
PR 18-AUG-1999. 99US-0149426.
PR 20-AUG-1999. 99US-0149722.
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PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
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PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 05-AUG-1999; 99US-0147192.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
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PR 21-JUL-1999; 99US-0144814.
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PR 22-JUL-1999; 99US-0145087.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 01-SEP-1999; 99US-0151930.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 48.3%; Score 747.5; DB 21; Length 363;

Best Local Similarity 53.9%; Pred No. 2.4e-70; Matches 166; Conservative 38; Mismatches 77; Indels 27; Gaps 8;

QY 7 SFADFLAGVAAIAISRTAVPIERVKLLIOVHASKOITA---DKQYKIIDCVWRIPK 63
DB 61 nfaldflimgvsavaektaapiervklllqnp--demikagrlsepykgidcfgrtlk 118
QY 64 EDEVLSEFMKGNLANVRYRPTQALNFAFDKYKQIIRLGVDKRTOPWRPFAGNLASGNA 123
DB 119 deqfsglwrgntanvlylftqalnfafkdytkrlfnfkdd-rdykwkfaqnlasgnaa 177
QY 124 GATSLCFVYPLDFARTRLAAD---VGKAGAEERFRLGDLVKIKYSDSICKLYOGFNVS 180
DB 178 gassllfvyldyartcrllandekaakkgggqfdglvdvyrkllktldglaglyrgfnls 237
QY 181 VCGIITRYRAAYRGITDTAK-----GMLPPKNTNHYISMIAQTYAVAVAGLSYPPDIYR 235
DB 238 cvgllyvrglylfglydsavkpvlltqldqdsffasfalgwvl---tngaglasypidtyr 293
QY 236 RRMMSQGRKRGTDIMYTGTLDCWRKLTARDEGGAFFKAGMSNVLRMGAFVLYVDEI- 294
DB 294 rrrmmmsgea---vkyslsdalkqllknegaksltkgaganllravagavlysgydklq 350
QY 295 -----KKY 297
DB 351 llvfgkky 358

Search completed: February 13, 2002, 09:33:12
Job time: 109 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 13, 2002, 09:34:15 ; Search time 55.37 Seconds
(without alignments)
787.234 Million cell updates/sec

Title: US-09-393-441-33
Perfect score: 1543
Sequence: 1 MTEQAISEAFADFLAGIAA.....LRGMAFVLVDELKKVI 298

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp_invertebrate:*
7: sp.mammal:*
8: sp_mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp_plant:*
12: sp_rhodent:*
13: sp_virus:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1422	92.2	298	6	046373
2	1421	92.1	298	13	0919M9
3	1418	91.9	298	11	062164
4	1409	91.3	298	13	09PRH1
5	1406	91.1	298	13	09PRH2
6	1402	90.9	298	13	09YIC4
7	1259	81.6	317	13	091336
8	1235.5	80.1	300	5	09NHM5
9	1187.5	77.0	288	5	044093
10	1183.5	76.7	288	5	044094
11	1176.5	76.2	304	5	025129
12	1137.5	73.7	307	5	062526
13	1119	72.5	315	4	09H0C2
14	1041	67.5	313	5	021103
15	1039	67.3	313	5	P91410
16	1038	67.3	300	5	045865
17	996	64.5	309	5	094740
18	993.5	64.4	300	5	001813
19	993	64.4	300	5	017407

20	973.5	63.1	318	5	09B36
21	946.5	61.3	307	8	09XM22
22	944	61.2	301	5	025692
23	943	61.1	301	5	026006
24	827	53.6	170	6	09XS69
25	778.5	50.5	305	3	09P8M1
26	764	49.5	326	5	P91270
27	760	49.3	307	5	076286
28	759	49.2	303	3	074260
29	756.5	49.0	306	5	016683
30	753	48.8	307	5	026697
31	750.5	48.6	385	10	09FY52
32	747	48.4	306	3	P78754
33	744	48.2	388	10	049875
34	743	48.2	379	10	049447
35	743	48.2	386	10	P93767
36	743	47.6	331	10	041628
37	731.5	47.4	305	3	09P876
38	731	47.4	317	5	09N647
39	728.5	47.2	305	3	09P875
40	688.5	44.6	330	10	09PM86
41	681.5	44.2	298	5	021809
42	653.5	42.4	262	10	09AVT6
43	520.5	33.7	327	10	09LF44
44	500.5	32.4	162	5	026130
45	441.5	28.6	158	5	076467

ALIGNMENTS

RESULT 1
ID 046373 PRELIMINARY: PRT: 298 AA.
AC 046373;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SKELETAL MUSCLE;
RA Yamaguchi N., Kasai M.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB009386; BA23777.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mitl_carrier.
DR Pfam: PF00153; mito_car1.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
SQ SEQUENCE 298 AA: 32901 MW: CAEA32C8B164AD78 CRC64;

Query Match 92.2% Score 1422; DB 6; Length 298;
Best Local Similarity 88.9%; Pred. No. 6.9e-122;
Matches 265; Conservative 20; Mismatches 13; Indels 0; Gaps 0;
QY 1 MTEQAISEAFADFLAGIAAISKTAAPIERVKLLQVQHASKOIADKQKGIQVDCIVR 60
DB 1 MSQQLSFLKDFLAGGAAVSVKTAAPIERVKLLQVQHASQISAEKQYKGIQVDCIVR 60
QY 61 IPEQGYLFWKRGNLNVIRYPTQALNFAFKQYKQIFLGGYDKHTQFRRYRAGNLASG 120
DB 61 IPEQGYLFWKRGNLNVIRYPTQALNFAFKQYKQIFLGGYDKHTQFRRYRAGNLASG 120

QY 121 GAAGATSLCFEYPLDFAFTRRLADYVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFEYPLDFAFTRRLADYVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
 QY 181 VGGIITVRAAFVGYVDYDKAGMLPDPKNTNHIYVSMIAOTVTVAAGVSPPTVRRMM 240
 DB 181 VGGIITVRAAFVGYVDYDKAGMLPDPKNTNHIYVSMIAOTVTVAAGVSPPTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIKIFRDEGGAFFKAGSNVLRGKGAFVLYLDELKVI 298
 DB 241 QSGRKADIMYTGTVDCMKRIKIFRDEGGAFFKAGSNVLRGKGAFVLYLDELKVI 298

RESULT 2
 Q919M9 PRELIMINARY: PRT: 298 AA.
 AC Q919M9:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADENINE NUCLEOTIDE TRANSLOCASE.
 GN ANTI.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
 OX Xenopodinae; Xenopus.
 NCBI_TaxID=83355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosrowshahian F., Varmuza S.L., Liversage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 Dynamic Patterns of Expression During Development."
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF231347; AAE63471.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 32940 MW; 91B740133751877F CRC64;

Query Match 92.1%; Score 1421; DB 13; Length 298;
 Best Local Similarity 90.3%; Pred. No. 8.6e-122;
 Matches 269; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADKQYGIYDCIYR 60
 DB 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADKQYGIYDCIYR 60
 QY 61 IPKEGVLSEFWGRLANVIRYPTQALNFAFDKKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 DB 61 IPKEGVLSEFWGRLANVIRYPTQALNFAFDKKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 QY 61 IPKEGVLSEFWGRLANVIRYPTQALNFAFDKKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 DB 61 IPKEGVLSEFWGRLANVIRYPTQALNFAFDKKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 QY 121 GAAGATSLCFEYPLDFAFTRRLADYVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFEYPLDFAFTRRLADYVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
 QY 181 VGGIITVRAAFVGYVDYDKAGMLPDPKNTNHIYVSMIAOTVTVAAGVSPPTVRRMM 240
 DB 181 VGGIITVRAAFVGYVDYDKAGMLPDPKNTNHIYVSMIAOTVTVAAGVSPPTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIKIFRDEGGAFFKAGSNVLRGKGAFVLYLDELKVI 298
 DB 241 QSGRKADIMYTGTVDCMKRIKIFRDEGGAFFKAGSNVLRGKGAFVLYLDELKVI 298

RESULT 3
 Q62164 PRELIMINARY: PRT: 298 AA.
 AC Q62164:
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADENINE NUCLEOTIDE CARRIER (ADENINE NUCLEOTIDE TRANSLOCASE 1) (SIMILAR
 TO SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ADENINE NUCLEOTIDE
 TRANSLATOR), MEMBER 4).
 DE SL25A4 OR MANCI OR ANTI.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE=MUSCLE;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes."
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: X74510; CA52616.1; -;
 DR EMBL: AF240002; AAE64470.1; -;
 DR EMBL: BC003791; AAH03791.1; -;
 DR MGD: MGI:1353495; Slc25a4.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match 91.9%; Score 1418; DB 11; Length 298;
 Best Local Similarity 88.9%; Pred. No. 1.6e-121;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADKQYGIYDCIYR 60
 DB 1 MTEQAISFAKDELAGIAAIAISKTAVAPIERVKLLQYOHASKQIADKQYGIYDCIYR 60
 QY 61 IPKEGVLSEFWGRLANVIRYPTQALNFAFDKKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 DB 61 IPKEGVLSEFWGRLANVIRYPTQALNFAFDKKYKQIFLGVDKHTQFWRYFAGNLNSG 120
 QY 121 GAAGATSLCFEYPLDFAFTRRLADYVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFEYPLDFAFTRRLADYVGKSGTEREFRGLDCLVKITKSDGIRGLYOGFSVS 180
 QY 181 VGGIITVRAAFVGYVDYDKAGMLPDPKNTNHIYVSMIAOTVTVAAGVSPPTVRRMM 240
 DB 181 VGGIITVRAAFVGYVDYDKAGMLPDPKNTNHIYVSMIAOTVTVAAGVSPPTVRRMM 240
 QY 241 QSGRKADIMYTGTVDCMKRIKIFRDEGGAFFKAGSNVLRGKGAFVLYLDELKVI 298
 DB 241 QSGRKADIMYTGTVDCMKRIKIFRDEGGAFFKAGSNVLRGKGAFVLYLDELKVI 298

RESULT 4
 Q9PRH1

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ID 09PRH1      PRELIMINARY:      PRT:      298 AA.
AC 09PRH1:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008463; BAA36513.1; -;
DR EMBL: AB008456; BAA36506.1; -;
DR EMBL: AB008461; BAA36511.1; -;
DR EMBL: AB008462; BAA36512.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mitc_carrier.
DR InterPro: IPR002030; Mitc_uncoupling.
DR Pfam: PF00153; mito_carrt. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F54BD36 CRC64;

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Query Match          91.3%; Score 1409; DB 13; Length 298;
Best Local Similarity 88.6%; Pred. No. 1.1e-120;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

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QY 1 MPEQAIKFAKDFLAGGIAAISTAVAPIERVKLLLOVQHASKQIADKQKIVDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDDAAISFAKDFLAGGVAIAISKTAAVAPIERVKLLLOVQHASKQIADKQKIMCIVR 60
QY 61 IPKEGVLSFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRVAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 IPKEGVLSFWKGNLANVIRFPTQALNFAFKDKYKIFLDVNDKRTQFWRVAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADAVKSGTEREFGIGDCLVKTITKSDGIRGLYOGFSYS 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GAAGATSLCFVYPLDFARTRLADAVKAGADREFKIGDCLAKIFKSDGIRGLYOGFNVS 180
QY 181 VGGITIIYRAAYFGVYDTAKGMLDPKKNTHIVSWMTAQVTAVAGVSYPFDTVRRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VGGITIIYRAAYFGIYDTAKMLDPKNTHTIFISWMTAQVTAVAGFASYPFDVRRRMM 240
QY 241 QSGRKADIMYTCVQWCKRIFRDEGKAFKFGAMSVNLKMGAGFVLVLYDELKTYI 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 QSGRKGAELMYSGTIDCKWKIARDEGSRAFKFGAMSVNLKMGAGFVLVLYDELKTYI 298

RESULT 5
09PRH2      PRELIMINARY:      PRT:      298 AA.
AC 09PRH2:
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008460; BAA36510.1; -;
DR EMBL: AB008458; BAA36508.1; -;
DR EMBL: AB008459; BAA36509.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mitc_carrier.
DR InterPro: IPR002030; Mitc_uncoupling.
DR Pfam: PF00153; mito_carrt. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33082 MW; B0E225E867599406 CRC64;

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Query Match          91.1%; Score 1406; DB 13; Length 298;
Best Local Similarity 88.3%; Pred. No. 2e-120;
Matches 263; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

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QY 1 MPEQAIKFAKDFLAGGIAAISTAVAPIERVKLLLOVQHASKQIADKQKIVDCIVR 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MDDAAISFAKDFLAGGVAIAISKTAAVAPIERVKLLLOVQHASKQIADKQKIMCIVR 60
QY 61 IPKEGVLSFWKGNLANVIRFPTQALNFAFKDKYKQIFLGVDKHTQFWRVAGNLASG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 IPKEGVLSFWKGNLANVIRFPTQALNFAFKDKYKIFLDVNDKRTQFWRVAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLADAVKSGTEREFGIGDCLVKTITKSDGIRGLYOGFSYS 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 GAAGATSLCFVYPLDFARTRLADAVKAGADREFKIGDCLAKIFKSDGIRGLYOGFNVS 180
QY 181 VGGITIIYRAAYFGVYDTAKGMLDPKKNTHIVSWMTAQVTAVAGVSYPFDTVRRRMM 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 VGGITIIYRAAYFGIYDTAKMLDPKNTHTIFISWMTAQVTAVAGFASYPFDVRRRMM 240
QY 241 QSGRKADIMYTCVQWCKRIFRDEGKAFKFGAMSVNLKMGAGFVLVLYDELKTYI 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 QSGRKGAELMYSGTIDCKWKIARDEGSRAFKFGAMSVNLKMGAGFVLVLYDELKTYI 298

RESULT 6
09YTIC4      PRELIMINARY:      PRT:      298 AA.
AC 09YTIC4:
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE ADP/ATP TRANSLOCASE.
OS Rana rugosa (Frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99083429; PubMed=9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase."
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN, MITOCHONDRIAL
CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.

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DR EMBL: AB008457; BAA36507.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 90.9%; Score 1402; DB 13; Length 298;
 Best Local Similarity 87.9%; Pred. No. 4.7e-120;
 Matches 262; Conservative 21; Mismatches 15; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERKLLQVQHASKOIADKQYKGYVDCIYR 60
 DB 1 MTDAAISFAKDFLAGGVAASIKTAIVAPIERKLLQVQHASKOITADKQYKGYMDCVYR 60
 OY 61 IPKEGVLSFWKGNLANIYRFPPTQALNFAFDKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 DB 61 IPKEGVLSFWKGNLANIYRFPPTQALNFAFDKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 OY 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 OY 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 OY 181 VOGIIYRAAFYGVYDTAKGMLPDPKNTHIYVSMIAQTVTAAGVSPEDTVRRMM 240
 DB 181 VOGIIYRAAFYGVYDTAKGMLPDPKNTHIYVSMIAQTVTAAGVSPEDTVRRMM 240
 OY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298
 DB 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298
 OY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298
 DB 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298

RESULT 7
 O91336 PRELIMINARY; PRT; 317 AA.

ID O91336
 AC O91336;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADP/ATP TRANSLOCASE.
 OS Rana sylvatica (wood frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cai O., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress";
 RL Biochim. Biophys. Acta 1353:69-78(1997).
 RN [2]
 RP REVISIONS.
 RA Cai O., Storey K.B.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: U44832; AAA97882.2; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 SQ SEQUENCE 317 AA; 35005 MW; 5f66B7EDBD5CB872 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;
 Best Local Similarity 86.8%; Pred. No. 6e-107;
 Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

OY 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERKLLQVQHASKOIADKQYKGYVDCIYR 60
 DB 1 MTDAAISFAKDFLAGGVAASIKTAIVAPIERKLLQVQHASKOITADKQYKGYMDCVYR 60
 OY 61 IPKEGVLSFWKGNLANIYRFPPTQALNFAFDKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 DB 61 IPKEGVLSFWKGNLANIYRFPPTQALNFAFDKDKYKQIFLGVDKHTQFMRYFAGNLSG 120
 OY 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 OY 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVS 180
 OY 181 VOGIIYRAAFYGVYDTAKGMLPDPKNTHIYVSMIAQTVTAAGVSPEDTVRRMM 240
 DB 181 VOGIIYRAAFYGVYDTAKGMLPDPKNTHIYVSMIAQTVTAAGVSPEDTVRRMM 240
 OY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298
 DB 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298
 OY 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298
 DB 241 OSGRKADIMTGTVDCKRKIFRDEGKAFKFGKAMSNVLKRGKGFVLVLDLKKVI 298

RESULT 8
 O9NHWS PRELIMINARY; PRT; 300 AA.

ID O9NHWS
 AC O9NHWS;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ADP/ATP TRANSLOCASE.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Oestridae; Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS MAL SEEKING;
 RA Chen Z., Fair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: AF218587; AA932322.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Inner membrane; Mitochondrion; Transport.
 SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;

Query Match 80.1%; Score 1235.5; DB 5; Length 300;
 Best Local Similarity 79.5%; Pred. No. 7.7e-105;
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;

OY 6 ISFAKDFLAGGIAAISKTAIVAPIERKLLQVQHASKOIADKQYKGYVDCIYR 65
 DB 9 LGFVDFDAAGGISAIVSTAIVAPIERKLLQVQHASKOISPDKGKIMDFVRIPEKQ 68
 OY 66 GVLFWKGNLANIYRFPPTQALNFAFDKDKYKQIFLGVDKHTQFMRYFAGNLSGAGA 125
 DB 69 GFAASYWGNMANVIYRFPPTQALNFAFDKDKYKQIFLGVDKHTQFMRYFAGNLSGAGA 128
 OY 126 TSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVSVOGII 185
 DB 129 TSLCFYVPLDFARTRLADYKSGTEREFGLDCLVKTIKSDGIRGLYOGFSVSVOGII 187

QY	186	IYRAAYFCVYDTAKGNLDPDKNTHTIVSVMMLAQVTAAGVSVSYPFDTVRRRMMSQGRK	245
DB	188	IYRAAYFCGYDARKMLLDPKNTPIYISMALAQVTTAAGIVSYPFDTVRRRMMSQGRK	247
QY	246	GADIMYGTGYDCKRKIFRDEGKAFKFGKAMSVNLKMGCAFVLYLYDELKRYE	298
DB	248	ATEIIYKNTLHCWATIAKQEGTGAFFKAFSVNLRTGTGAFVLYLYDEIKKFL	300
RESULT	9		
ID	044093	PRELIMINARY;	PRT; 288 AA.
AC	044093;		
DT	01-JUN-1998	(TREMBLrel, 06, Created)	
DT	01-JUN-1998	(TREMBLrel, 06, last sequence update)	
DT	01-JUN-2001	(TREMBLrel, 17, last annotation update)	
DE	ADP/ATP TRANSLOCASE (FRAGMENT).		
GN	SESB.		
OC	Drosophila pseudoobscura (fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7237;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Zeng L.-W., Cameron J.M., Chen B., Kreitman M.;		
RL	Genetica 0:0-0(1997).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL		
CC	INNER MEMBRANE (BY SIMILARITY).		
CC	-1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.		
DR	EMBL; AF025798; AAB87883.1; -.		
DR	FLYbase; FBgn0023292; Dpse\esb.		
DR	InterPro; IPR001993; Mitoch_carrier.		
DR	InterPro; IPR002067; Mit_carrier.		
DR	Pfam; PF00153; mito_carri. 3.		
DR	PRINTS; PR00926; MITOCH_CARRIER.		
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.		
DR	Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.		
KW	NON_TER		
FT	288		
SQ	SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;		
	Query Match	77.0%; Score 1187.5; DB 5; Length 288;	
	Best Local Similarity	80.7%; Pred. No. 1.8e-100;	
	Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;		
QY	5	AISFKDFIAGGIIAAISTAVAPIERKLLIQVOHASKQIADKQYGIYCIIVRIPE	64
DB	7	AIGFKDKDRAGGISAAVSKTAVAPIERKLLIQVOHISKQISPDQYKGMVDCFRIRPE	66
QY	65	QGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDYKHTQFWRYFAGNLASGAAG	124
DB	67	QGFSSFWKGNLANVIRYPTQALNFAFKDKYKQVFLGVDKNTQFWRYFAGNLASGAAG	126
QY	125	ATSLCFEYVPLDPAFRLAADVGSKSTEREERELGSCIVYKTSDDIRGLYQSFVSQGI	184
DB	127	ATSLCFEYVPLDPAFRLAADVGSKG-QREFGLGKCLTKITFSDGLVGLYRGFVSQGI	185
QY	185	IYRAAYGCVYDTAAGMLPDKNTHTIVSVMMLAQVTTAAGVSVSYPFDTVRRRMMSQGR	244
DB	186	IYRAAYGCVYDTAR-MLPDKNTHTIVSVMMLAQVTTAAGVSVSYPFDTVRRRMMSQGR	244
QY	245	KGADIMYGTGYDCKRKIFRDEGKAFKFGKAMSVNLKMGCAFVLY	289
DB	245	KATEIIYKNTLHCWATIAKQEGTGAFFKAFSVNLRTGTGAFVLY	288
RESULT	10		
ID	044094	PRELIMINARY;	PRT; 288 AA.
AC	044094;		
DT	01-JUN-1998	(TREMBLrel, 06, Created)	

Query Match	76.7%	Score 1183.5	DB 5	Length 288
Best Local Similarity	80.4%	Pred. No. 4.1e-100		
Matches 229	Conservative 20	Mismatches 33	Indels 3	Gaps 3
QY 5	AISFAKDELAGGIAAIAISKTAVAPIERVKLLQVQHASKOIAADKQYKGIYDCIVIRPKE 64			
DB 7	AMGFVKDFDAAGGISAAVSKTAVAPIERVKLLQVQHISKQISPDQKQYKGMVDCFIIRPKE 66			
QY 65	QGVLSFWMGNIANVIRYRPTQALNFAFDKTKQITLGGVDKHTQWRFFAGNLASGGAAG 124			
DB 67	QGFSEFWMGNIANVIRYRPTQALNFAFDKTKQYVFLGGVDKHTQWRFFEMGLASGGAAG 126			
QY 125	ATSLCFVYPLDFAPRIRLADYKSGSTEREFRLGDLVTKIFKPSDRIRLYOGFSVYOGI 184			
DB 127	ATSLCFVYPLDFAPRIRLADYDKGS-QKEPFGSLGCLTKIRKSDLVYLRKGFVYOGI 185			
QY 185	IYRAAYFGVYDTAKGLPDKPNTIIVYSWMAIAQTVAVAGVSYFPDTRRRMMQSGR 244			
DB 186	IYRAAYFGVYDTAR-MLPDKPNTIYISMAIAQCVTTVAGIVSYFPDTRRRMMQSGR 244			
QY 245	KGADINMYGTVDQWKRIFRDEGKAFKFFGANSNVLRGNGAFVLY 289			
DB 245	KATELIYKNTIHCWGTIAKQE-GTAFKFGAASNVLRGTGAFVLY 288			
RESULT 11				
ID 225129	PRELIMINARY:	PRT:	304 AA.	
AC Q25129				
DT 01-NOV-1996	(TREMBLrel. 01, Created)			
DT 01-NOV-1996	(TREMBLrel. 01, Last sequence update)			
DT 01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE ADP/ATP TRANSLOCASE.				
GN HRAUTL1.				
OS Halocynthia roretzi (Sea squirt).				
OC Eukaryota, Metazoa, Chordata, Urochordata; Ascidiacea;				
OC Stolidobranchia; Pyuridae; Halocynthia.				
OX NCBI_TaxID=7729;				
RN 11	SEQUENCE FROM N.A.			
RA	Miya T.;			
RL	Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.			
RN 12				
RP	SEQUENCE FROM N.A.			
RA	Miya T., Makabe K., Satcho N.;			

RT "Expression of a gene for major mitochondrial protein, ADP/ATP
 RT translocase, during embryogenesis in the ascidian *Halogethella*
 RT *roretzi*."
 RL Dev. Growth Differ. 36:39-48(1994).
 CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -I- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: D83069; BA01765.1; -
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carrt. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 DR SEQUENCE 304 AA; 33306 MW; 51FDD07D6B654880 CRC64;
 SQ
 Query Match 76.2%; Score 1176.5; DB 5; Length 304;
 Best Local Similarity 75.8%; Pred. No. 1.9e-99;
 Matches 226; Conservative 20; Mismatches 51; Indels 1; Gaps 1;
 QY 1 MTEQATSPAKDLGAGIAAISKTAAPLERVKLLQYOHASKOIAADKQYGVDCIYR 60
 D6 1 MPMASVADRAKDLAIGTSTAALISKITVAPLERVKLLQYQAVSTQKAGTEYGIIDAIVR 60
 QY 61 IPKEGVLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 120
 D6 61 IPKEGVLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 120
 QY 121 GAAGTATSCFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 180
 D6 121 GAAGTATSCFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 180
 QY 121 GAAGTATSCFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 180
 D6 121 GAAGTATSCFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 180
 QY 181 VGGITTYRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMM 240
 D6 181 VGGITTYRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMM 240
 QY 180 IGGITTYRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMM 239
 D6 180 IGGITTYRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMM 239
 QY 241 QSGRKADIMVTGIVDCMKRIFRDEGKAFFKGAWSNVLRGKGFVLYVDELKVI 298
 D6 241 QSGRKADIMVTGIVDCMKRIFRDEGKAFFKGAWSNVLRGKGFVLYVDELKVI 298
 QY 240 QSGRKADIMVTGIVDCMKRIFRDEGKAFFKGAWSNVLRGKGFVLYVDELKVI 297
 D6 240 QSGRKADIMVTGIVDCMKRIFRDEGKAFFKGAWSNVLRGKGFVLYVDELKVI 297
 RESULT 12
 ID 062526 PRELIMINARY; PRT; 307 AA.
 AC 062526;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ANT2 PROTEIN.
 GN ANT2 OR CG1683.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 CX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.R., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu N., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jimmel B.E., Kodish C., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasok P., Lei Y., Levitsky A.A., Li Z., Li Z., Liang Y., Lin X.,
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacled J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RA Zhang Y.O., Davis A.W., Roote J., Ashburner M.;
 RL Submitted (May-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AE003484; AA047956.1; -
 DR EMBL: Y10618; CAA71629.1; -
 DR FlyBase: FBgn002511; Ant2.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mlt_carrier.
 DR Pfam: PF00153; mito_carrt. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.
 DR SEQUENCE 307 AA; 33744 MW; 3D6B3D6D82061C0C CRC64;
 SQ
 Query Match 73.7%; Score 1137.5; DB 5; Length 307;
 Best Local Similarity 74.8%; Pred. No. 7.2e-96;
 Matches 217; Conservative 26; Mismatches 46; Indels 1; Gaps 1;
 QY 7 SFAPKFLAGGIAAISKTAAPLERVKLLQYOHASKOIAADKQYGVDCIYRIPKDG 66
 D6 7 SFAPKFLAGGIAAISKTAAPLERVKLLQYOHASKOIAADKQYGVDCIYRIPKDG 66
 QY 17 SFLPMFMGVSAAIAKTAAPLERVKLLQYQAVSTQKAGTEYGIIDAIVR 76
 D6 17 SFLPMFMGVSAAIAKTAAPLERVKLLQYQAVSTQKAGTEYGIIDAIVR 76
 QY 67 VLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 126
 D6 67 VLSFWRGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 126
 QY 77 FSSFWKGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 136
 D6 77 FSSFWKGNLANVIRFFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLSAG 136
 QY 127 SLCEFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 186
 D6 127 SLCEFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 186
 QY 137 SLCEFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 195
 D6 137 SLCEFYVPLDFATRLADYKSGTEREPFGDCLVTKTKSDICRLYGFVS 195
 QY 187 YRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMMQSGRG 246
 D6 187 YRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMMQSGRG 246
 QY 196 YRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMMQSGRG 255
 D6 196 YRAAYGVVDYFAKGLPDKNTHIVSWMIAGTVAVAGVSPFTVRRMMQSGRG 255
 QY 247 ADIMVTGIVDCMKRIFRDEGKAFFKGAWSNVLRGKGFVLYVDELKVI 296
 D6 247 ADIMVTGIVDCMKRIFRDEGKAFFKGAWSNVLRGKGFVLYVDELKVI 296
 QY 256 SBMYKNTAHKWLIVAKOEGIAFKAALSNIRCTGALVLYALYDEK 305
 D6 256 SBMYKNTAHKWLIVAKOEGIAFKAALSNIRCTGALVLYALYDEK 305
 RESULT 13
 ID 09H0C2 PRELIMINARY; PRT; 315 AA.
 AC 09H0C2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Geisel C., Steilyes L.;
 RL Submitted (Jan-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL; 080931; AAB38001.1; -;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Inner membrane; Mitochondrion; Repeat; Transmembrane; Transport.
 KW SEQUENCE 313 AA; 34356 MW; CF07C473A719CCB6 CRC64;

* Query Match 67.3%; Score 1039; DB 5; Length 313;

Best Local Similarity 70.9%; Pred. No. 7.4e-87;
 Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

OY 8 FAKDPLAGGIAAIAISKTAVAPIERYKLLQVQHASKOIAADKQYKGIYDCIVIRPEQGV 67
 DB 25 FLIDLASGTAATAVSKTAVAPIERYKLLQVQDASLTITADKRYGIYDVLRVPKEQGY 84
 OY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLAGSAGAGATS 127
 DB 85 AALMRGNLANVIRYPTQALNFAFKDYKNIFQKGLDKKRDWKFAGNLAGSAGAGATS 144
 OY 128 LCFVYPLDFARTLAADYKSGTEREERGLDCLVKTFTKSDGIRGLYOGFSYVOGIITY 187
 DB 145 LCFVYPLDFARTLAADYKKA-NEKEFKGLADCLVKAISDGPITGLYRGFEYSVOGIITY 203
 OY 168 RAAVFGVYDTAKGML-PPEKNTHTIVSWMIAGTVTAAGVSVYPTVYRRMMQSGRKG 246
 DB 204 RAAVFGMEDTAKMFTADGKILNFAAAMIAQVTVGSGILSYPMVDYVRRMMQSGRK- 262
 OY 247 ADIMYTGIVDCRRKIFRDEGGAFFKAGMSNVLKMGGAFLVLYDELKVI 298
 DB 263 -DVLKNTGLDCAVKIIEKMGSMFKGALSNVFGTGGALVLAIFYDEIQFTI 313

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 Job time: 172 sec